

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 8, 2005, 17:33:48 ; Search time 8749 Seconds  
(without alignments)  
11043.514 Million cell updates/sec

Title: US-09-377-795-1  
Perfect score: 1994  
Sequence: 1 ggacagcatggcccttgt.....gtaaaaaaaaaaaaaaaa 1994

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb\_ba:\*
- 2: gb\_hg:\*
- 3: gb\_in:\*
- 4: gb\_ov:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_bts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1994	100.0	1994	9	AF074382	Homo sapi
2	1898.6	95.2	2071	9	BC012114	Homo sapi
3	1885.6	94.6	2073	9	AY114157	Homo sapi
4	1850.4	92.8	1966	9	BC000299	Homo sapi
5	1848.4	92.7	1990	9	BC050612	Homo sapi
6	1836.4	92.1	2035	9	AF091453	Homo sapi
7	1836.4	92.1	2121	9	AF261086	Homo sapi
8	1832.6	91.9	1975	9	AF062089	Homo sapi
9	1823	91.4	2009	6	BD135431	Receptor
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11	1823	91.4	2009	6	AR534835	Sequence
12	1823	91.4	2009	6	AX017214	Sequence
13	1757.2	88.1	2034	6	BD135432	Receptor
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16	1757.2	88.1	2034	6	AX017215	Sequence
17	1358.6	68.1	2038	6	AX781112	Sequence
18	1235.4	62.0	1666	9	AK000593	Homo sapi
19	1021.6	51.2	2175	4	BTA414557	Bos tauri

20	945.6	47.4	1798	10	AF513109	Mus muscu
21	943.6	47.3	2250	10	AY112937	Mus muscu
22	940.4	47.2	1874	6	AR454143	Sequence
23	938.2	47.1	1748	10	AF069542	Mus muscu
24	927.6	46.5	2282	10	BC021431	Mus muscu
25	902.4	45.3	1239	10	AY392762	Rattus no
26	705.8	35.4	23106	9	HSA271718	Homo sapi
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33	701	35.2	155221	2	AC145688	Pan trogl
34	656.4	32.9	136551	2	AC149258	Papio anu
35	656.4	32.9	148309	2	AC146529	Papio anu
36	656.4	32.9	165013	2	AC149865	Papio anu
37	656.4	32.9	178507	2	AC146312	Macaca mu
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ALIGNMENTS

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DEFINITION  
AF074382 1994 bp mRNA linear PRI 15-JUN-2001  
cds.  
ACCESSION AF074382  
VERSION AF074382.1 GI:3641279  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Rothwarf,D.M., Zandi,E., Natoli,G. and Karin,M.  
TITLE IKK-gamma is an essential regulatory subunit of the IkkappaB kinase complex  
JOURNAL Nature 395 (5699), 297-300 (1998)  
MEDLINE 98421680  
PUBMED 9751060

REFERENCE  
AUTHORS Rothwarf,D.M., Zandi,E., Natoli,G. and Karin,M.  
TITLE Direct Submission  
JOURNAL Submitted (25-JUN-1998) Pharmacology, University of California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0636, USA

FEATURES

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## ORIGIN

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	Matches 1994;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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DB	1	GGCAGCAGCATGGCCCTTGTGATCCAGGTGGGGAACCTAAGGCCCCAGAGAAGTCAAGACC	60						
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QY	181	TCAGATGTGACGCCCAAGTGTGGCCCGGACAGATCAGAGCATCTGGGCCGAAGATC	240						
DB	181	TCAGATGTGACGCCCAAGTGTGGCCCGGACAGATCAGAGCATCTGGGCCGAAGATC	240						
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DB	241	TCCTCTGGGGAAGCCAGCCATGTGACCTTGCCTTTCAGAACAGGCGCTCTCCAGACCT	300						
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RESULT 2
BC012114
LOCUS
DEFINITION
Homo sapiens inhibitor of kappa light polypeptide gene enhancer in
B-cells, kinase-gamma, mRNA (cDNA clone MGC:20127 IMAGE:4651870),
complete cds.
ACCESSION
BC012114
VERSION
BC012114.1 GI:15082398
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2071)
AUTHORS
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalls, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 2071)
Strausberg, R.
Direct Submission
Submitted (02-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywicki, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Fawan Pandoh, Anna-Lisa Prabhu, Farvaneh Saeedi, Jacqueline
Schein, Duane Smalus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Teai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 29 Row: 0 Column: 12
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DB 74 GCAGACTATCAATCCAGTCTTCTCCCTCACTCCCTGTGAAGCTCTCCAGCATCATGA 133
QY 123 GGTCCCATCAG----- 133
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ORIGIN

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QY	358	GATTCGCGGAGCGCTGAGGAGCTCTGATTTTCAAGCCAGCAGAGGAGGAGAA	417
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QY	538	ATGCCAGCAGCAGATGGCTGAGGACAAAGCCCTCTGTGAAGCCAGGTGACCTCTTGTCT	597
DB	614	ATGCCAGCAGCAGATGGCTGAGGACAAAGCCCTCTGTGAAGCCAGGTGACCTCTTGTCT	673
QY	598	CGGGAGCTGACGAGGAGCAGAGTCTGCTTGGAGGTGCGCACTAAGGAATGCCAGGCTCT	657
DB	674	CGGGAGCTGACGAGGAGCAGAGTCTGCTTGGAGGTGCGCACTAAGGAATGCCAGGCTCT	733
QY	658	GGAGGCTCGGGCCCGGGCCGAGCAGAGCAGGCGGCGAGCTGAGAGTGAAGCGGAGGC	717
DB	734	GGAGGCTCGGGCCCGGGCCGAGCAGAGCAGGCGGCGAGCTGAGAGTGAAGCGGAGGC	793
QY	718	GCTGACAGCAGCAGCAGAGTGCAGTGCAGCTGCGCATGCGAGGCCAGAGCGTGA	777
DB	794	GCTGACAGCAGCAGCAGAGTGCAGTGCAGCTGCGCATGCGAGGCCAGAGCGTGA	853
QY	778	GGCCCGCTCTCCGATGAGCGCCAGCCCTCTGGAGGAGAGAGGAAGCTGGCCAGTT	837
DB	854	GGCCCGCTCTCCGATGAGCGCCAGCCCTCTGGAGGAGAGAGGAAGCTGGCCAGTT	913
QY	838	GCAGTGGCTATCACCACTCTTCCAGAAATACGACAAACCAATCAAGAGCAGCGTGT	897
DB	914	GCAGTGGCTATCACCACTCTTCCAGAAATACGACAAACCAATCAAGAGCAGCGTGT	973

QY	898	GGCAGTTCAGCGAAGCGAGAAATCAGCTGGAAGATCTCAAAACAGCAGCTCCAGCAGC	957
DB	974	GGCAGTTCAGCGAAGCGAGAAATCAGCTGGAAGATCTCAAAACAGCAGCTCCAGCAGC	1033
QY	958	CGAGAGCCCTGTGGCCAAACAGAGGTGATGATTAAGCTGAAGGAGGAGCGGAGCA	1017
DB	1034	CGAGAGCCCTGTGGCCAAACAGAGGTGATGATTAAGCTGAAGGAGGAGCGGAGCA	1093
QY	1018	GCACAAGATTGTGATGGAGACCGTTCCGTTGATGAGGCCAGGCGGATATCTACAGGC	1077
DB	1094	GCACAAGATTGTGATGGAGACCGTTCCGTTGATGAGGCCAGGCGGATATCTACAGGC	1153
QY	1078	GGACTTCCAGGCTGAGAGCAGGCCCGGAGAAAGCTGGCCGAGAGAGAGAGTCTCTGCA	1137
DB	1154	GGACTTCCAGGCTGAGAGCAGGCCCGGAGAAAGCTGGCCGAGAGAGAGAGTCTCTGCA	1213
QY	1138	GGAGCAGTGGAGCAGCTTCAGAGGAGGTACAGCAAACTGAAGGCCAGCTGTCAAGAGTC	1197
DB	1214	GGAGCAGTGGAGCAGCTTCAGAGGAGGTACAGCAAACTGAAGGCCAGCTGTCAAGAGTC	1273
QY	1198	GGCAGAGATTCAGGACATGAGGAAGCGGATGTGAGGTCTCCAGGCCCTCTTGCCCCC	1257
DB	1274	GGCAGAGATTCAGGACATGAGGAAGCGGATGTGAGGTCTCCAGGCCCTCTTGCCCCC	1333
QY	1258	CGCCCTCTGCTACCTCTCTCTCCCTGCGCCCTGCGCAGCAGAGAGAGAGCCGCCGA	1317
DB	1334	CGCCCTCTGCTACCTCTCTCTCCCTGCGCCCTGCGCAGCAGAGAGAGAGCCGCCGA	1393
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QY	1738	TCTCAGGAGAACTGCTTCCCTTCGACAGCTGGGGTGGCAGCTCTTCTCCACCGGACA	1797
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DB	1933	TCCTTTTGGGCTGATGCTATTTCCATTTTGCAGCAGACCGATGTGTATTTAAACAGTCA	1992
QY	1918	CTATTGATGGACATTTGGGTTGTTTCCCATCTTTTGTGTACCATAAATATGGCATAGTA	1977
DB	1993	CTATTGATGGACATTTGGGTTGTTTCCCATCTTTTGTGTACCATAAATATGGCATAGTA	2052

QY 1978 AAAA 1981  
 Db 2053 AAAA 2056

RESULT 4  
 BC000299  
 LOCUS  
 DEFINITION Homo sapiens inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma, mRNA (CDNA clone MGC:8374 IMAGE:2820134), complete cds.

ACCESSION BC000299  
 VERSION BC000299.2 GI:33875269  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1966)  
 AUTHORS Strausberg, R.L., Collins, F.S., Wagner, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L.H., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heish, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, L., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shvachenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalilus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257  
 PUBMED 12477932

REFERENCE 2 (bases 1 to 1966)  
 AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 On Aug 19, 2003 this sequence version replaced gi:12653066.  
 Contact: MGC help desk  
 Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)  
 Tissue Procurement: DCTD/DRP  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: [nisc\\_mgc@hgr.nih.gov](mailto:nisc_mgc@hgr.nih.gov)  
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgon, C., Voet, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 1 Row: c Column: 5

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21361093.

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 Best Local Similarity 99.9%; Pred. No. 3.1e-301;  
 Matches 1862; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
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 Db 103 CAGCCCTTCCTCCCTGTTGGATGATAGGACCTCTGGAAGACCACTGTGTGAGATGGTG 162  
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Db	583	GAGAGCCAGAGTCCGCTTTGGAGGCTGCCACTAAGGAAATGCCAGGCTCTGAGAGGGTTCGGGCC	642
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Qy	1331	TTCTGCTGTCCCAAGTGCCAGTAGTACAGGCCCTTGATATGACACCCCTGCAAGATACATGTC	1390
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Db	1602	TCGCTGCTCTTTTGTTCCTCTCTGCTCGAACAACCTTGGCTCGGGCTAATCCCTCC	1661
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Db	1662	CTCTTCCTCCACCCGGCACCTGGGGAAGTCAAGAAATGGGGCTCTCAGGAGAAC	1721
Qy	1751	TGCTTCCCTCGGCAGAGCTGGGTGGCAGCTCTTCCTCCACCGGACACCGACCGCCGC	1810
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Qy	1931	TTTGGGTGTTTCCCATCTTTTGTACCATAAATAATGTCATAGTAAAAA	1990
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Qy	1991	AAAA 1994	
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RESULT 5			
BC050612			
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DEFINITION	Homo sapiens inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma, mRNA (cDNA clone MGC:60070 IMAGE:6062527), complete cds.		
ACCESSION	BC050612		
VERSION	BC050612.2	GI:34193533	
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1990)		
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.F., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.M., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haie, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raja, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Viallalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99 (26), 16899-16903	(2002)
MEDLINE	22388257		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 1990)		
AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (08-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>		
COMMENT	On Aug 25, 2003 this sequence version replaced gi:29792041.		



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Db	709	GGGCGGCCAGCAGCAGCGCGGCGAGCTGGAGAGTGAGCGCGCGCTGCGAGCAGCAGC	768
QY	732	ACAGCGTCAGGTGACCAAGCTGCGCATGCGAGGCGCAGAGCGTGGAGGCGCGCTCCGCA	791
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ORIGIN

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Query Match      91.9%; Score 1832.6; DB 9; Length 1975;
Best Local Similarity 99.7%; Pred. No. 3e-298;
Matches 1846; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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QY 191 CAGCCAGTGTGGCCCGCAGCAGATCAGACGTACTGGCGGAGAGTCTCTCTGGGG 250
DB 153 CAGCCAGTGTGGCCCGCAGCAGATCAGACGTACTGGCGGAGAGTCTCTCTGGGG 212

QY 251 AAGCCAGCATGCTGCACCTGCTTCAGAAAGAGGCGCTCTGAGACCCCTCCAGCGCTGC 310
DB 213 AAGCCAGCATGCTGCACCTGCTTCAGAAAGAGGCGCTCTGAGACCCCTCCAGCGCTGC 272

QY 311 CTGGAGGAGATCAAGAGCTCGAGATCCGATCCGCGAGAGCAACCCAGATTTCTGCGGGAG 370
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QY 371 CGCTCGGAGGAGCTTCTGCATTTCCAGCCAGCAGAGAGGAGAGAGTTCCTCATG 430
DB 333 CGCTCGGAGGAGCTTCTGCATTTCCAGCCAGCAGAGAGGAGAGAGTTCCTCATG 392

QY 431 TGCAGATTTCCAGGAGGCGAGGAACTGCTGGAGAGACTCGGCCCTGGAGAGCTCGATCTG 490
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QY 491 AAGAGCGAGAGGAGCAGGCTCTCGGAGGTGGAGCACTTGAAGAGATGCCAGCAGCAG 550
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QY 911 AAGCCAGGAGATCGAGCTGGAAGATCTCAAAACAGCAGCTCCAGCAGGCGCGAGGAGGCCCTG 970
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RESULT 9  
BD135431  
LOCUS  
DEFINITION

BD135431 2009 bp DNA linear PAT 18-SEP-2002  
Receptor function regulator for TNF/NGF receptor family and other

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ACCESSION	BD135431	protein.	
VERSION	BD135431.1	GI:23230376	
KEYWORDS	JP 2002506644-A/1.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 2009)		
AUTHORS	Wallach,D., Kovalenko,A., Horwitz,M.S. and Li,Y.		
TITLE	Receptor function regulator for TNF/NGF receptor family and other proteins		
JOURNAL	Patent: JP 2002506644-A 1 05-MAR-2002; YEDA RESEARCH AND DEVELOPMENT CO LTD, ALBERT EINSTEIN COLLEGE OF MEDICINE		
COMMENT	OS Homo sapiens (human) PN JP 2002506644-A/1 PD 05-MAR-2002 PR 18-MAR-1999 JP 2000536855 PR 19-MAR-1998 IL 123758,01-SEP-1998 IL 126024 PI DAVID WALLACH,ANDREI KOVALENKO,MARSHALL S HORWITZ,YONGAN LI PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P29/00,A61P31/18, PC A61P35/00, PC C07K14/47,C07K16/18,C12N1/21,C12P21/02//C07K14/525,C07K14/715, PC C12N15/00, PC A61K37/02 CC Receptor function regulator for TNF/NGF receptor family and other proteins FH Key Location/Qualifiers FT source 1..2009 FT /organism='Homo sapiens (human)'. FT Location/Qualifiers 1..2009 /organism='Homo sapiens' /mol_type='genomic DNA' /db_xref='taxon:9606'		
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ORIGIN			
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QY	311	CTGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACAGATTCTGGGGAG	370
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DB	496	AAGAGGCAAGAGGAGCAGGCTCTGGGGAGGTGGAGCACTCAAGAGATGCCAGAGCAG	555
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LOCUS AR534835 2009 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 1 from patent US 6734174.  
ACCESSION AR534835  
VERSION AR534835.1 GI:53925507  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2009)  
AUTHORS Wallach,D., Kovalenko,A., Horwitz,M.S. and Li,Y.  
TITLE Modulators of the function of receptors of the TNF/NGF receptor  
JOURNAL Patent: US 6734174-A 11-MAY-2004;  
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Best Local Similarity 99.6%; Pred. No. 1.2e-296;  
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Db 316 CTGGAGGAGAAATCAAGAGCTCCAGATGCCATCCGCGCAGAGCAACAGATTTCTGGGG 375  
Qy 371 CGCTCGAGGAGCTTCTGCAATTTCAAGCCAGCAGAGGAGGAGAGAGTTCCTCATG 430  
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RESULT 12  
AX017214 2009 bp DNA linear PAT 07-SEP-2000  
LOCUS Sequence 1 from Patent WO9947672.  
DEFINITION AX017214  
ACCESSION AX017214  
VERSION AX017214.1 GI:10042134  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Wallach,D., Kovalenko,A., Li,Y. and Horwitz,M.S.  
TITLE Modulators of the function of receptors of the tnfr/ngf receptor  
JOURNAL family and other proteins  
Patent: WO 9947672-A 1 23-SEP-1999;  
WALLACH DAVID (IL); YEDA RES & DEV (IL); KOVALENKO ANDREI (IL);  
EINSTEIN COLL MED (US); LI YONGAN (US); HORWITZ MARSHALL S (US)  
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Best Local Similarity 99.6%; Pred. No. 1.2e-296;  
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## FEATURES

source

Location/Qualifiers

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Best Local Similarity 98.3%; Pred. No. 1.4e-285;  
Matches 1826; Conservative 3; Mismatches 21; Indels 8; Gaps 5;

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 Keywords Homo sapiens (human)  
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REFERENCE  
 AUTHORS Wallach,D. and Kovalenko,A.  
 TITLE Modulators of receptors of the tnfrngf receptor family  
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 YEDA RESEARCH & DEVELOPMENT COMPANY, LTD. (IL)  
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 Query Match 88.1%; Score 1757.2; DB 6; Length 2034;  
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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.



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Db 1415 ATGTATGAGGTGATTCAGTAGGGCGGCGCAGTGAAGGCCACTGCTGCCCGGAGGACG 1473
QY 1446 TCCCGGGACCGTGAGTCTGGCTTCTCTCCCGCTGCTAGCCAGGATGAAGGGC 1505
Db 1474 TCCCGGGACCGTGAGTCTGGCTTCTCTCCCGCTGCTAGCCAGGATGAAGGGC 1533
QY 1506 TGGGTGGCCACACTGGGATGCCACTGGAGCCCAAGGAGGAGCTGGCCGCGCAGCTT 1565
Db 1534 TGGGTGGCCACACTGGGATGCCACTGGAGCCCAAGGAGGAGCTGGCCGCGCAGCTT 1593
QY 1566 AGCTTTCAGCTGTGA-TCCGCTGGTCCCTCTTTTGGGGTAGATGGGCCCGCATCAGG 1624
Db 1594 AGCTTTCAGCTGTGTATTCGCTGGTCCCTCTTTTGGGGTAGATGGGCCCGCATCAGG 1653
QY 1625 CCGTACTCGCTGCTCTTTTGTTCCTTCTGTCTGCTGAAACCACTTGCCTCGGGCTAAT 1684
Db 1654 CCGTACTCGCTGCTCTTTTGTTCCTTCTGTCTGCTGAAACCACTTGCCTCGGGCTAAT 1713
QY 1685 CCCTCCCTCTCCCTCAGCGGCACTGGGAGTCAAGATGGGGCTGGGGCTCTCAGG 1744
Db 1714 CCCTCCCTCTCCCTCAGCGGCACTGGGAGTCAAGATGGGGCTGGGGCTCTCAGG 1773
QY 1745 GAGAACTGCTTCCCTGGCAGAGCTGGGTGGCAGCTCTTCTCCCAAGGAGACCCGACCC 1804
Db 1774 GAGAACTGCTTCCCTGGCAGAGCTGGGTGGCAGCTCTTCTCCCAAGGAGACCCGACCC 1833
QY 1805 GCCCGCCGCTGTGCCCTGGGAGTGTGCCCTCTTACCATGACACGGGTGCTCTCCTTTT 1864
Db 1834 GCCCGCCGCTGTGCCCTGGGAGTGTGCCCTCTTACCATGACACGGGTGCTCTCCTTTT 1893
QY 1865 GGGCTGCAATGCTATTTCATTTTGAGCCAGACCGATGTGATTTAAACAGTCACTATTGA 1924
Db 1894 GGGCTGCAATGCTATTTCATTTTGAGCCAGACCGATGTGATTTAAACAGTCACTATTGA 1953
QY 1925 TGGACATTGGGTGTTTCCCATCTTTTGTATACATAAATAATGGCATAGTAAAAA 1982
Db 1954 TGGACATTGGGTGTTTCCCATCTTTTGTATACATAAATAATGGCATAGTAAAAA 2011
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Search completed: February 9, 2005, 01:01:06







Query Match		88.1%;	Score 1757.2;	DB 4;	Length 2034;				
Best Local Similarity		98.3%;	Pred. No. 0;						
Matches 1826;		Conservative	3;	Mismatches	21;	Indels	8;	Gaps	5;
QY	132	AGCCCTTGGCCCTGTTGGATGAATAGGACACTCTGGAGAGCCAACTGTGTGAGATGGTGC	191						
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QY	192	AGCCAGTGTGTCGCGCCGCGAGCATGAGAGCTACTGCGGCGAAGAGTCTCTCTGGGGA	251						
DB	215	AGCCAGTGTGTCGCGCCGCGAGCATGAGAGCTACTGCGGCGAAGAGTCTCTCTGGGGA	274						
QY	252	AGCCAGCATGTCTGACCTCTCAGAACAGGCGCTCTCAGACCTCTCAGCGCTGCC	311						
DB	275	AGCCAGCATGTCTGACCTCTCAGAACAGGCGCTCTCAGACCTCTCAGCGCTGCC	334						
QY	312	T-GGAGGAGATCAAGAGCTCCGAGATCCATCCCGCAG-AGCAACACAGATTCTTCGCGGA	369						
DB	335	TGGAGGAGATCAAGAGCTCCGAGATCCATCCCGCAGTACACACAGATTCTTCGCGG	394						
QY	370	GCCTCGGAGGAGCTTCTGC-ATTTCCAGCCAGCCAGGAGGAGAGAGATTTC	425						
DB	395	AGCTCGGAGGAGGAGCTTCTGCATTTTCCAAAGCCAGCCAGAGGAGGAGAGATTTC	454						
QY	426	TCATGTCAAGTTTCCAGAGGCGCAGGAACTGGTGGAGAGCTCGGCTCGAGAGCTCG	485						
DB	455	TCATGTCAAGTTTCCAGAGGCGCAGGAACTGGTGGAGAGCTCGGCTCGAGAGCTCG	514						
QY	486	ATCTGAAGGCGAAGAGAGAGGCTCTGCGGAGGTTGAGCACTCTGAAGAGATGCCAGC	545						
DB	515	ATCTGAAGGCGAAGAGAGAGGCTCTGCGGAGGTTGAGCACTCTGAAGAGATGCCAGC	574						
QY	546	AGCAGATGCTGAGGACAGGCTCTGTGAAGCCAGGTCAGCTCTTCTCGGGAGC	605						
DB	575	AGCAGATGCTGAGGACAGGCTCTGTGAAGCCAGGTCAGCTCTTGTCTCGGGAGC	634						
QY	606	TGAGGAGAGCCAGAGTCTGAGGCTGCGCACTTAAGAAATGCCAGGCTCTGAGGCTC	665						
DB	635	TGAGGAGAGCCAGAGTCTGAGGCTGCGCACTTAAGAAATGCCAGGCTCTGAGGCTC	694						
QY	666	GGCCCGGCGCCAGCAGAGGCGCGGAGCTGTGAGAGTGAGCGAGCGCTGCGAGC	725						
DB	695	GGCCCGGCGCCAGCAGAGGCGCGGAGCTGTGAGAGTGAGCGAGCGCTGCGAGC	754						
QY	726	AGCAGCACAGCTGAGGTGAGCAGCTGCGCATGSCAGGCGCAGAGCGTGGAGCCGCGC	785						
DB	755	AGCAGCACAGCTGAGGTGAGCAGCTGCGCATGSCAGGCGCAGAGCGTGGAGCCGCGC	814						
QY	786	TCCGATGAGCGCCAGGCGCGCTCGGAGGAGAGAGAGCTGGCCAGTTGCGAGTGG	845						
DB	815	TCCGATGAGCGCCAGGCGCGCTCGGAGGAGAGAGAGCTGGCCAGTTGCGAGTGG	874						
QY	846	CTATCACAGCTCTCCAGAGTACGACACACCATCAAGAGCAGCGTGGTGGGAGTG	905						
DB	875	CTATCACAGCTCTCTCAAGAAATACGACACCATCAAGAGCAGCGTGGTGGGAGTG	934						
QY	906	AGCGAAGCGAGGATGAGGTGGAAGATCTCAACAGCAGCTCCAGCAGCGCGAGGAGG	965						
DB	935	AGCGAAGCGAGGATGAGGTGGAAGATCTCAACAGCAGCTCCAGCAGCGCGAGGAGG	994						
QY	966	CCCTGGTCCCAACAGAGAGTGATCGATAAGCTGAAGAGAGGCGCGAGCAGCAAGA	1025						
DB	995	CCCTGGTCCCAACAGAGAGTGATCGATAAGCTGAAGAGAGGCGCGAGCAGCAAGA	1054						
QY	1026	TTGTGATGAGACCTTCCGCTGTGAGGCGCCAGGCGATATCTCAAGCGGACTTCC	1085						
DB	1055	TTGTGATGAGACCTTCCGCTGTGAGGCGCCAGGCGATATCTCAAGCGGACTTCC	1114						
QY	1086	AGGCTGAGAGGAGCGCCCGGAGAGCTGGCCGAGAGAGAGAGCTCTCTGAGGAGCAGC	1145						
DB	1115	AGGCTGAGAGGAGCGCCCGGAGAGCTGGCCGAGAGAGAGAGCTCTCTGAGGAGCAGC	1174						
QY	1146	TGAGCAGCTGAGAGGAGGTACAGCAACTGAAGGCCAGCTGTGAGGAGTCCGCCAGGA	1205						

DB	1175	TGGAGCAGCTGCGAGAGGAGGTACAGCAAACTGAAGGCCAGCTGTGAGAGTCGGCCAGGA	1234
QY	1206	TCGAGGACATGAGGAAGCGGCATGTGAGAGTCTCCAGGCCCTTGGCCCCCGCCCTG	1265
DB	1235	TCGAGGACATGAGGAAGCGGCATGTGAGAGTCTCCAGGCCCTTGGCCCCCGCCCTG	1294
QY	1266	CCTACCTCTCTCTCCCTGCGCCCTGCGCCAGCAGAGAGAGAGGCCCGCCGAGGAGCCAC	1325
DB	1295	CCTACCTCTCTCTCCCTGCGCCCTGCGCCAGCAGAGAGAGAGGCCCGCCGAGGAGCCAC	1354
QY	1326	CTGACTTCTGCTGTCCCAAGTGCAGATCATGAGGCCCTGTATATGAGACACCTGTGAGATAC	1385
DB	1355	CTGACTTCTGCTGTCCCAAGTGCAGATCATGAGGCCCTGTATATGAGACACCTGTGAGATAC	1414
QY	1386	ATGTCATGAGAGTGCATTGAGTAGGGCGCGCAGTGCAAGGCCACTGCTGCGCCGAGGAGC	1445
DB	1415	ATGTCATGAGAGTGCATTGAGTAGGGCGCGCAGTGCAAGGCCACTGCTGCGCCGAGGAGC	1473
QY	1446	TGCCCGGGAACGCTGCACTGTGCGCTTCTCTCCGCGCTGCTAGCCAGGATGAAGGCC	1505
DB	1474	TGCCCGGGAACGCTGCACTGTGCGCTTCTCTCCGCGCTGCTAGCCAGGATGAAGGCC	1533
QY	1506	TGGGTGSCCAAACTGGGATGCCACTTGGAGCCCGCCAGCAGGAGCTGGCCCGGACCTT	1565
DB	1534	TGGGTGSCCAAACTGGGATGCCACTTGGAGCCCGCCAGCAGGAGCTGGCCCGGACCTT	1593
QY	1566	ACGCTTCAGCTGTGA-TCCGCTGGTGGTCTCTTTTGGGGTAGATGCGGCCCGATCAGG	1624
DB	1594	ACGCTTCAGCTGTGTGATTGCTGGTGGTCTCTTTTGGGGTAGATGCGGCCCGATCAGG	1653
QY	1625	CCTGACTGCTGCTCTTTTGTTCCTTCTGCTGTCTGCAACCACTTGCCTCGGGCTAAT	1684
DB	1654	CCTGACTGCTGCTCTTTTGTTCCTTCTGCTGTCTGCAACCACTTGCCTCGGGCTAAT	1713
QY	1685	CCCTCCCTCTTCTCCACCGGCACCTGGGAGTCAAGAAATGGGGCTGGGGCTCTCAGG	1744
DB	1714	CCCTCCCTCTTCTCCACCGGCACCTGGGAGTCAAGAAATGGGGCTGGGGCTCTCAGG	1773
QY	1745	GAGAACTGCTTCCCTTGGCAGAGCTGGGTGGCAGCTTCTCCCTCCACCGGACACCGACCC	1804
DB	1774	GAGAACTGCTTCCCTTGGCAGAGCTGGGTGGCAGCTTCTCCCTCCACCGGACACCGACCC	1833
QY	1805	GGCCGCGCTGTGCGCTGGGAGTGTGCTCTTACCATGCAACGCGTGTCTCTCTTTT	1864
DB	1834	GGCCGCTGTGCGCTGGGAGTGTGCTCTTACCATGCAACGCGTGTCTCTCTTTT	1893
QY	1865	GGGCTGCATGCTATTCATTTTGCAGCCAGACCGATGTGTATTTAAACAGTCACTATTGA	1924
DB	1894	GGGCTGCATGCTATTCATTTTGCAGCCAGACCGATGTGTATTTAAACAGTCACTATTGA	1953
QY	1925	TGAGCAATTTGGGTGTGTTTCCCATCTTTTGTACCAATAATAATGCGATAGTAAAAA	1982
DB	1954	TGAGCAATTTGGGTGTGTTTCCCATCTTTTGTACCAATAATAATGCGATAGTAAAAA	2011

RESULT 4  
US-09-253-701-2  
; Sequence 2, Application US/09253701  
; Patent No. 6680366  
; GENERAL INFORMATION:  
; APPLICANT: SHOJI, YAMAKA  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCE ENCODING A MODULATOR OF NF-KB  
; FILE REFERENCE: 0660-0146-55  
; CURRENT APPLICATION NUMBER: US/09/253,701  
; CURRENT FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 1874  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-253-701-2















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; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-620-925-1

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Query Match	6.9%	Score 137;	DB 3;	Length 9600;
Best Local Similarity	48.4%;	Pred. No. 4e-20;		
Matches 380;	Conservative 0;	Mismatches 405;	Indels 0;	Gaps 0;
QY	475	GGAGAACTCGATCTGAAGAGGCAAGAGGACAGCGCTCTGCGGAGGTGGAGCACTTAA	534	
DB	706	GCAGGACGGAGGGCAGGNGCAGGAGGGGCAGGACGAGGAGGGGCAGGACGAGGA	765	
QY	535	GAGATGCCAGCAGCAGATGGCTGAGGACAAGCCCTCTGTGAAGCCACAGGTGACGTCCTT	594	
DB	766	GGAGGGGCAGAGGGGGCAGGAGGGGCAGGAGGGGCAGGACGAGGAGGAGGGCAGGAGCA	825	
QY	595	GCTCGGGAGCTGCAGGAGACCCAGAGTCTGCTTGAGGCTGCCACTAAGGATGCCAGGC	654	
DB	826	GGAGGAGGGCAGGAGGGGCAGGAGGGGCAGGACGAGGAGGGGCAGGACGAGGAGGA	885	
QY	655	TCTTGGAGGGTCGGGCCCGGCCAGCAGCAGCGCGCGCAGCTGGAGAGTGAAGCCCGA	714	
DB	886	GGGGCAGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGACGAG	945	
QY	715	GGCGCTGCAGCAGCAGCAGCAGCTGCTGAGTGTGACCACTGGCCTGCAGGGCCAGCGGT	774	
DB	946	GGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGACGAGGAGGGGCAGGAGG	1005	
QY	775	GGAGGGCGCGCTCCGATCGAGCGCCAGGCGCGCTCGGAGGAGGAAGAGCTTGGCCCA	834	
DB	1006	GCAGGAGGGCAGGAGCAGGAGGAGGGGCAGGACGAGGAGGGGCAGGAGGGGCAGGAGGG	1065	
QY	835	GTTTGCAGGTGGCCTATCACCACTCTTCCAAAGATACGACAAACACATCAAGAGCAGCGT	894	
DB	1066	GCAGGAGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGGCA	1125	
QY	895	GGTGGGCAGTGAAGCGGAGGAGGAGTGCAGCTGGAAGATCTCAACACAGCAGCTCCAGCA	954	
DB	1126	GGAGGGCAGGAGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGGG	1185	
QY	955	GGCCGAGGAGGCCCTGTGTGCCAAACAGGAGGTGATCGATAGCTGAAGGAGGAGGCCGA	1014	
DB	1186	GCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAG	1245	
QY	1015	GCAGCACAAGTTGTGATGAGACCGTTCGCGTCTGAAGGCCAGCGCGATATCTACAA	1074	
DB	1246	GGAGGGGCAGGAGGGGCAGGAGCAGGAGGAGGGGCAGGAGGGGCAGGAGGGGCAGGAGGGGC	1305	
QY	1075	GGCGGACTTCCAGGCTGAGAGGAGGCGGCCCGGAGAGCTGCGCCGAGGAAGAGAGTCTCT	1134	
DB	1306	GGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGGGCAGGA	1365	
QY	1135	GCAGGAGCAGCTGGAGCAGCTGCAGAGGGAGTACAGCAAACTGAAGGCCAGCTGTGAGGA	1194	
DB	1366	GCAGGAGGAGGGGCAGGAGCAGGAGGGGCAGGAGGAGTGAAGGCCGGGGTCGAGGA	1425	
QY	1195	GTCGGCCAGGATCGAGGACATGAGGAAGCGGCATGTCGAGGTCTCCACAGGCCCTTTGCC	1254	
DB	1426	GGCAGTGGAGGCCGGGGTCAAGAGGTAGTGTGAGGCCCGGGTTCAGAGAGGTAGTGTGAGGC	1485	
QY	1255	CCCCG	1259	
DB	1486	CGCCG	1490	

RESULT 14  
US-07-884-811-15  
; Sequence 15, Application US/07884811  
; Patent No. 5316921  
; GENERAL INFORMATION:  
; APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R.  
; TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS  
; NUMBER OF SEQUENCES: 21

```

CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/884,811
FILING DATE: 19920518
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 755.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 10596 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-884-811-15

Query Match 6.9%; Score 137; DB 1; Length 10596;
Best Local Similarity 48.4%; Pred. No. 4.1e-20;
Matches 380; Conservative 0; Mismatches 405; Indels 0; Gaps 0;

QY 475 GGAGNAGCTCGATCTGNAAGAGCAGAGGAGCAGAGGCTCTCGGGAGGTGGAGCACCTGAA 534
Db 2240 GCAGGACGGGAGGGGCGAGGAGCAGAGGGGGCAGGAGCAGAGGGGGCAGGAGCAGGA 2299
QY 535 GAGATGCCAGCAGCAGATGGCTCAGGACAAGGCTCTGTGAAAGCCACAGTGACGTCCTT 594
Db 2300 GGAGGGGCAGAGGGGCGAGAGGGGGCAGGAGGAGGGGCGAGAGCA 2359
QY 595 GCTCGGGAGCTGCAGAGAGCCAGAGTGCCTTTGGAGGCTGCCACTAAGGAATGCCAGGC 654
Db 2360 GGAGAGGGGGCAGAGGGGGCAGAGGGGCGAGGAGCAGGAGGAGGGGCGAGGAGCAGGA 2419
QY 655 TCTTGGAGGTCTGGGCGCGGCGCCACGAGCAGGCGCGGCGAGCTGGAGAGTTCAGCGCA 714
Db 2420 GGGGCGAGGGGGCGAGGAGCAGGAGGAGGGGGCAGGAGGGGGCAGGAGGGGGCAGGAG 2479
QY 715 GGCCTGTCAGCAGCAGCAGCAGCTGCAGGTGGACCAAGCTGCGCATCGAGGGCCAGAGCGT 774
Db 2480 GGAGGGGCAGAGCAGAGAGGGGGCAGAGGGGGCAGGAGCAGGAGGAGGGGCGAGGGG 2539
QY 775 GGAGGGCCGCGCTCCGCATGGAGCCAGGCGCGCTTCGGAGGAGGAAGAGGAGCTGGCCCA 834
Db 2540 GCAGGAGGGGCAGGAGCAGGAGGAGGGGCGAGGAGGAGGGGGCAGGAGGGGCGAGGG 2599
QY 835 GTTTCAGGTTGGCTTATCACCAGCTCTTCCAGAAATACGACAACCATCAAGAGCAGCGT 894
Db 2600 GCAGGAGCAGGAGGGGCGAGGAGCAGGAGGAGGGGGCAGGAGGGGGCAGGAGGGGGCAG 2659
QY 895 GGTGGGCGAGTGAGCGGAGCGAGGAATGAGCTGGGAAGATCTCAACAGCAGCTCCAGCA 954
Db 2660 GSAAGGGGCGAGGAGCAGAGGGGGCAGGAGCAGGAGGGGGCAGGAGGAGGGGCGAGGG 2719
QY 955 GGCCCGAGGAGGCCCTGCTGGCCCAAACAGGAGGTGATCGATTAAGCTGAAGGAGGAGCCCA 1014

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[illegible]

Db	1201	CAGGATCGAGGACATGAGGAGAGCGCGATGTCGAGGTCTCCAGGCGCCCTTGCCCCCGCG	1260
Qy	1261	CCCTGCTACTCTCTCTCCCTGCGCCCTGCCAGCCAGAGAGAGGCCCCCGGAGGA	1320
Db	1361	CCCTGCTACTCTCTCTCTCCCTGCGCCCTGCCAGCCAGAGAGAGGCCCCCGGAGGA	1320
Qy	1321	GCCACCTGACTTCTGCTGTCTCCCAAGTGCCAGTATCAGGCGCCCTGATATGACACCCCTGCA	1380
Db	1321	GCCACCTGACTTCTGCTGTCTCCCAAGTGCCAGTATCAGGCGCCCTGATATGACACCCCTGCA	1380
Qy	1381	GATACATGTATGGAGTGCATTTGAGTAGGGCGGGCCAGTGCAGAGGCACCTGCTGCCCGA	1440
Db	1381	GATACATGTATGGAGTGCATTTGAGTAGGGCGGGCCAGTGCAGAGGCACCTGCTGCCCGA	1440
Qy	1441	GGAGTSCCGGAGACGTGCAGTCTCGCTTTCTCTCCGCTGCTAGTGCACAGATGA	1500
Db	1441	GGAGTSCCGGAGACGTGCAGTCTCGCTTTCTCTCCGCTGCTAGTGCACAGATGA	1500
Qy	1501	AGGCTGGGTGGCCACAACCTGGGATCCACTTGGAGCCCAACCAGGAGTGGCGCCGCGC	1560
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Qy	1561	ACCTTAGCTTTCAGCTGTTGATCCGTGCTGCTCTCTTTGGGTAGATGCGGCCCGCGAT	1620
Db	1561	ACCTTAGCTTTCAGCTGTTGATCCGTGCTGCTCTCTTTGGGTAGATGCGGCCCGCGAT	1620
Qy	1621	CAGGCTTGACTCGCTGCTCTTTTGTTCCTCTCTGCTCTCGAACCACTTGCTCTCGGGC	1680
Db	1621	CAGGCTTGACTCGCTGCTCTTTTGTTCCTCTCTGCTCTCGAACCACTTGCTCTCGGGC	1680
Qy	1681	TAATTCCTTCCTCTTCTCTCAACCGGCACTGGGGAGTCAAGATGGGGCCTTGGGCTCT	1740
Db	1681	TAATTCCTTCCTCTTCTCTCAACCGGCACTGGGGAGTCAAGATGGGGCCTTGGGCTCT	1740
Qy	1741	CAGGAGAACTGCTTCCCTGCGAGAGCTGGGTGGGAGCTCTTCCTCCACCGGACACCG	1800
Db	1741	CAGGAGAACTGCTTCCCTGCGAGAGCTGGGTGGGAGCTCTTCCTCCACCGGACACCG	1800
Qy	1801	ACCGCGCGCGCTGTGCCCTGGGAGTGTGCCCTCTTACCATGCACACGGGTGCTCTCC	1860
Db	1801	ACCGCGCGCGCTGTGCCCTGGGAGTGTGCCCTCTTACCATGCACACGGGTGCTCTCC	1860
Qy	1861	TTTTGGGCTGCATGCTATTTCGATTTTGGAGCAGACCGATGTATTAAACGAGTCACTA	1920
Db	1861	TTTTGGGCTGCATGCTATTTCGATTTTGGAGCAGACCGATGTATTAAACGAGTCACTA	1920
Qy	1921	TTGATGCAATTTGGGTGTGTTTTCCCATCTTTTGTATTACCATAAATAGGCAATAGTAAAA	1980
Db	1921	TTGATGCAATTTGGGTGTGTTTTCCCATCTTTTGTATTACCATAAATAGGCAATAGTAAAA	1980
Qy	1981	AAAAAAAAAAAAA 1994	
Db	1981	AAAAAAAAAAAAA 1994	

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RESULT 2
US/09-851-673-1
; Sequence 1, Application US/09851673
; Publication No. US20030165985A1
; GENERAL INFORMATION:
; APPLICANT: Derry, Jonathan
; APPLICANT: Fauslow, William
; APPLICANT: Dougall, William
; TITLE OF INVENTION: SCREENING ASSAYS FOR
; FILE REFERENCE: 3198
; CURRENT APPLICATION NUMBER: US/09/851,673
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1994
; TYPE: DNA
; ORGANISM: Homo sapiens

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FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (149)...(1405)  
US-09-851-673-1

Query Match 100.0%; Score 1994; DB 10; Length 1994;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACAGCATGGCCCTTGTGATCCAGGTGGGGAACTAAGGCCAGAGAAAGTGGAGCC 60  
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QY 1 GGCACAGCATGGCCCTTGTGATCCAGGTGGGGAACTAAGGCCAGAGAAAGTGGAGCC 60  
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QY 61 CGCGACATATCAATCCCACTCTCTCCCTCACTCCCTGTGAAGCTCTCCAGCATCATC 120  
Db |||||  
QY 61 CGCGACATATCAATCCCACTCTCTCCCTCACTCCCTGTGAAGCTCTCCAGCATCATC 120  
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QY 121 GAGTCCCATACGCCCTTCCCTGTGGATGAATAGGACCTCTGGAAGAGCAACTGTG 180  
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QY 301 CCAGCGCTGCCTGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGCGCAGAGCAACAGAT 360  
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QY 661 GGGTCCGGCCCGGGCGCCAGCAGCAGCGCGGCGAGCTGGAGTGAAGCGAGCGCT 720  
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QY 841 GGTGGCCTATCACCAGCTCTTCCAAGATACGACCAACCAATCAAGAGCAGCGTGGTGG 900  
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QY 901 CAGTGCAGCGAAGCGAGGAATGAGCTGGAAAGTCTCAAAACAGCGCTCCAGAGGCCGA 960  
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QY 901 CAGTGCAGCGAAGCGAGGAATGAGCTGGAAAGTCTCAAAACAGCGCTCCAGAGGCCGA 960  
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QY 961 GGAGGCCCTGGTGGCCAAACAGAGGTGATCGATAGCTGAAGGAGGAGGCCGAGCAGCA 1020  
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QY 961 GGAGGCCCTGGTGGCCAAACAGAGGTGATCGATAGCTGAAGGAGGAGGCCGAGCAGCA 1020  
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QY 1021 CAAGATTGTGATGGAGACCGTTCCGGTGTGAAGGCCCAAGCGGATATCTCAAGCGGA 1080  
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QY 1021 CAAGATTGTGATGGAGACCGTTCCGGTGTGAAGGCCCAAGCGGATATCTCAAGCGGA 1080  
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QY 1081 CTTCCAGGCTGAGAGGCGCGGAGGAGCTGGCCGAGAGAGAGAGCTCTCTGAGGA 1140  
Db |||||  
QY 1081 CTTCCAGGCTGAGAGGCGCGGAGGAGCTGGCCGAGAGAGAGAGCTCTCTGAGGA 1140  
Db |||||  
QY 1141 GCAGCTGGAGCAGCTGCGAGGAGGTACAGCAAACTGAAGGCCAGCTGTCAAGAGTCGGC 1200  
Db |||||  
QY 1141 GCAGCTGGAGCAGCTGCGAGGAGGTACAGCAAACTGAAGGCCAGCTGTCAAGAGTCGGC 1200  
Db |||||  
QY 1201 CAGGATCGAGGACATGAGGAAGCGCATGTGAGGTCTCCAGGGCCCCCTTGCCCCCCGC 1260  
Db |||||  
QY 1201 CAGGATCGAGGACATGAGGAAGCGCATGTGAGGTCTCCAGGGCCCCCTTGCCCCCCGC 1260  
Db |||||  
QY 1261 CCCTGCTACCTCTCTCTCCCTGGCCCTGCCAGCAGAGAGAGAGAGAGAGAGAGAG 1320  
Db |||||  
QY 1261 CCCTGCTACCTCTCTCTCCCTGGCCCTGCCAGCAGAGAGAGAGAGAGAGAGAGAG 1320  
Db |||||  
QY 1321 GCACCTGACTTCTGTCTGCCCAAGTGCAGTATCAGGGCCCTGTATATGACACCCCTGCA 1380  
Db |||||  
QY 1321 GCACCTGACTTCTGTCTGCCCAAGTGCAGTATCAGGGCCCTGTATATGACACCCCTGCA 1380  
Db |||||  
QY 1381 GATACATGTCATGAGAGTGCATTTAGTAGGGCCGGCCAGTGCAGAGGCCACTTGCTGCCGA 1440  
Db |||||  
QY 1381 GATACATGTCATGAGAGTGCATTTAGTAGGGCCGGCCAGTGCAGAGGCCACTTGCTGCCGA 1440  
Db |||||  
QY 1441 GGAAGTCCCGGAGCCGTCAGTCTGCGCTTCTCTCCCGCTGCTAGCCAGAGATGA 1500  
Db |||||  
QY 1441 GGAAGTCCCGGAGCCGTCAGTCTGCGCTTCTCTCCCGCTGCTAGCCAGAGATGA 1500  
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QY 1501 AGGGCTGGGTGGCCCAACTGGGATGCCACTGGAGCCCCCAGCAGGAGCTGGCCCGGC 1560  
Db |||||  
QY 1501 AGGGCTGGGTGGCCCAACTGGGATGCCACTGGAGCCCCCAGCAGGAGCTGGCCCGGC 1560  
Db |||||  
QY 1561 ACCTTACGCTTCAGCTGTGATCCGCTGCTCCCTCTTTTGGGGTAGATGCGGCCCGAT 1620  
Db |||||  
QY 1561 ACCTTACGCTTCAGCTGTGATCCGCTGCTCCCTCTTTTGGGGTAGATGCGGCCCGAT 1620  
Db |||||  
QY 1621 CAGGCTGACTGCTGCTCTTTTGTTCCTTCTGCTGCTGCAACCACTTGCTCGGC 1680  
Db |||||  
QY 1621 CAGGCTGACTGCTGCTCTTTTGTTCCTTCTGCTGCTGCAACCACTTGCTCGGC 1680  
Db |||||  
QY 1681 TAATCCCTCCCTCTTCTCCACCCGCACTGGGGAGTCAAGAAATGGGGCTTGGGGCTCT 1740  
Db |||||  
QY 1681 TAATCCCTCCCTCTTCTCCACCCGCACTGGGGAGTCAAGAAATGGGGCTTGGGGCTCT 1740  
Db |||||  
QY 1741 CAGGAGAACTGCTTCCCTTGGCAGAGCTGGGTGGAGCTTCTTCTCCACCGGACACCG 1800  
Db |||||  
QY 1741 CAGGAGAACTGCTTCCCTTGGCAGAGCTGGGTGGAGCTTCTTCTCCACCGGACACCG 1800  
Db |||||  
QY 1801 ACCCGCCGCGCTGTCGCTGGGAGTGTGCCCTTTTACCATGACACAGGCTGCTCTCC 1860  
Db |||||  
QY 1801 ACCCGCCGCGCTGTCGCTGGGAGTGTGCCCTTTTACCATGACACAGGCTGCTCTCC 1860  
Db |||||  
QY 1861 TTTTGGGCTGCATGCTATTTCATTTTGCAGCCAGACCGATGTATTTAAACAGTCACTA 1920  
Db |||||  
QY 1861 TTTTGGGCTGCATGCTATTTCATTTTGCAGCCAGACCGATGTATTTAAACAGTCACTA 1920  
Db |||||  
QY 1921 TTGATGGAATTTGGTGTGTTTCCCATCTTTTGTTCATTAATTAATAGGATAGTAAAA 1980  
Db |||||  
QY 1921 TTGATGGAATTTGGTGTGTTTCCCATCTTTTGTTCATTAATTAATAGGATAGTAAAA 1980  
Db |||||  
QY 1981 AAAAAAAAAAAAAA 1994  
Db |||||  
QY 1981 AAAAAAAAAAAAAA 1994  
Db |||||

RESULT 3

US-10-628-841-3

; Sequence 3, Application US/10628841

; Publication No. US20040023918A1

; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia

; APPLICANT: Jacqueline Wyatt

; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-GAMMA EXPRESSION

; FILE REFERENCE: RTS-0191

; CURRENT APPLICATION NUMBER: US/10/628,841

; CURRENT FILING DATE: 2003-07-28

; PRIOR APPLICATION NUMBER: US/09/972,607

; PRIOR FILING DATE: 2001-10-06

; NUMBER OF SEQ ID NOS: 88

; SEQ ID NO 3

; LENGTH: 1994

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (149)...(1408)

US-10-628-841-3

Query Match 100.0%; Score 1994; DB 17; Length 1994;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCACGAGCATGGCCCTTGTGATCCAGGTGGGGAAACTAAGGCCCCAGAGAAGTGGAGACC 60

Db 1 GGCACGAGCATGGCCCTTGTGATCCAGGTGGGGAAACTAAGGCCCCAGAGAAGTGGAGACC 60

Qy 61 CCGCAGACTATCAATCCACGTCTCTTCCCCTCACTCCCTGTGAAGCTCTCCAGCATCATC 120

Db 61 CCGCAGACTATCAATCCACGTCTCTTCCCCTCACTCCCTGTGAAGCTCTCCAGCATCATC 120

Qy 121 GAGTCCCATCAGCCCTTGGCCCTTGGATGAATAGGCACCTCTGGAAGAGCCAACTGTG 180

Db 121 GAGTCCCATCAGCCCTTGGCCCTTGGATGAATAGGCACCTCTGGAAGAGCCAACTGTG 180

Qy 181 TGAGATGGTGCACGCCAGTGGTGGCCCGCAGCAGATCAGGAGTACTGGGCGAAGAGTC 240

Db 181 TGAGATGGTGCACGCCAGTGGTGGCCCGCAGCAGATCAGGAGTACTGGGCGAAGAGTC 240

Qy 241 TCCTCTGGGAAAGCCAGCCATGCTGCACCTCTTCAGAAACAGGGCGCTCCTGAGACCCCT 300

Db 241 TCCTCTGGGAAAGCCAGCCATGCTGCACCTCTTCAGAAACAGGGCGCTCCTGAGACCCCT 300

Qy 301 CCAGCGCTGCTCGAGGAGGAATCAAGAGCTCCGAGATGCCATCCGCGAGAGCAACAGAT 360

Db 301 CCAGCGCTGCTCGAGGAGGAATCAAGAGCTCCGAGATGCCATCCGCGAGAGCAACAGAT 360

Qy 361 TCTGCGGAGCGCTGGAGAGCTTCTGCACTTTCAGAGCCAGCCAGAGGAGAGAGA 420

Db 361 TCTGCGGAGCGCTGGAGAGCTTCTGCACTTTCAGAGCCAGCCAGAGGAGAGAGA 420

Qy 421 GTTCTCATGTGCAAGTTTCAGAGGCCAGGAAACTGTGTGAGAGACTCGGCGCTGGAGAA 480

Db 421 GTTCTCATGTGCAAGTTTCAGAGGCCAGGAAACTGTGTGAGAGACTCGGCGCTGGAGAA 480

Qy 481 GCTCGACTCTGAAGAGCAGAGGAGCAGCTCTGCGGGAGGTGGAGCACTCAAGAGATG 540

Db 481 GCTCGACTCTGAAGAGCAGAGGAGCAGCTCTGCGGGAGGTGGAGCACTCAAGAGATG 540

Qy 541 CAGCAGCAGATGGCTGAGGACAAGGCCCTCTGTGAAAGCCCAAGGTGAAGCTCTGCTCGG 600

Db 541 CAGCAGCAGATGGCTGAGGACAAGGCCCTCTGTGAAAGCCCAAGGTGAAGCTCTGCTCGG 600

Qy 601 GGAGCTGCGAGGAGCCAGAGTCGCTTGGAGCTGCCACTAAGGAATGCCAGGCTCTGGA 660

Db 601 GGAGCTGCGAGGAGCCAGAGTCGCTTGGAGCTGCCACTAAGGAATGCCAGGCTCTGGA 660

Qy 661 GGATCGGGCCCGGGCGGCCAGCGAGCAGCGCGCAGCTGGAGAGTGAAGCGGCGCT 720

QY 1801 ACCCGCCCGCGCTGTGCTGGAGTGTGCTGCCCTCTTACCATGCACAGGGTGTCTCC 1860  
DB 1801 ACCCGCCCGCGCTGTGCTGGAGTGTGCTGCCCTCTTACCATGCACAGGGTGTCTCC 1860  
QY 1861 TTTTGGGCTGCATGTATTCATTTTTCAGCCAGACCGATGTGTATTTAACAGTCACTA 1920  
DB 1861 TTTTGGGCTGCATGTATTCATTTTTCAGCCAGACCGATGTGTATTTAACAGTCACTA 1920  
QY 1921 TTGATGCATTTGGGTTGTTTCCCATCTTTTGTATACCATATAATAGGATAGTAA 1980  
DB 1921 TTGATGCATTTGGGTTGTTTCCCATCTTTTGTATACCATATAATAGGATAGTAA 1980  
QY 1981 AAAAAAAAAAAAAA 1994  
DB 1981 AAAAAAAAAAAAAA 1994

RESULT 4  
US-09-863-049A-3  
; Sequence 3. Application US/09863049A  
; Publication No. US2003002055A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenrick, Sue J.  
; APPLICANT: Nelson, David L.  
; APPLICANT: Aradhya, Swaroop  
; APPLICANT: D'Urso, Michele  
; APPLICANT: Woffendin, Hayley  
; APPLICANT: Munnich, Arnold  
; APPLICANT: Smahi, Asmaa  
; APPLICANT: Israel, Alain  
; APPLICANT: Poustka, Annemarie  
; APPLICANT: Lewis, Richard A  
; APPLICANT: Levy, Moise  
; APPLICANT: Heiss, Nina  
; TITLE OF INVENTION: Diagnosis and Treatment of Medical Conditions Associated with Def  
; FILE REFERENCE: NF-KAPPA B (NF-kB) Activation  
; CURRENT APPLICATION NUMBER: US/09/863, 049A  
; CURRENT FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/206,223  
; PRIOR FILING DATE: 2000-05-22  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2035  
; TYPE: DNA  
; ORGANISM: Human  
US-09-863-049A-3

Query Match 92.1%; Score 1836.4; DB 10; Length 2035;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1848; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
QY 132 AGCCCTTGCCCTGTGGATGAATAGGACCTCTGGAAGACCACTGTGTGAGATGGTGC 191  
DB 169 AGCCCTTGCCCTGTGGATGAATAGGACCTCTGGAAGACCACTGTGTGAGATGGTGC 228  
QY 192 AGCCAGTGTGGCCCGGAGAGATCAGAGATGTAAGAGAGAGAGTCTCTCTGGGGA 251  
DB 229 AGCCAGTGTGGCCCGGAGAGATCAGAGATGTAAGAGAGAGAGTCTCTCTGGGGA 288  
QY 252 AGCCAGCATGTGCACCTCCCTTCAGAACAGGGCGCTCTGAGACCTCCAGCGCTGCC 311  
DB 289 AGCCAGCATGTGCACCTCCCTTCAGAACAGGGCGCTCTGAGACCTCCAGCGCTGCC 348  
QY 312 TGGAGGAGATCAAGAGCTCCGAGATGCCATCCGGCAGACCAACAGATTTCTGCGGGAGC 371  
DB 349 TGGAGGAGATCAAGAGCTCCGAGATGCCATCCGGCAGACCAACAGATTTCTGCGGGAGC 408  
QY 372 GTTCGAGAGCTTTGCAATTTCCAAAGCAGGAGGAGAGAGGAGTTCTCATGT 431  
DB 409 GTTCGAGAGCTTTGCAATTTCCAAAGCAGGAGGAGGAGGAGTTCTCATGT 468

QY 432 GCAAGTTCAGAGAGCCAGGAACTGTGTGAGAGACTCGGCCCTGGAGAGCTCGATCTGA 491  
DB 469 GCAAGTTCAGAGAGCCAGGAACTGTGTGAGAGACTCGGCCCTGGAGAGCTCGATCTGA 528  
QY 492 AGAGCAGAAAGAGAGCAGGCTCTGCGGGAGGTGGAGCACTGAAGAGATGCCAGCAGCAGA 551  
DB 529 AGAGCAGAAAGAGAGCAGGCTCTGCGGGAGGTGGAGCACTGAAGAGATGCCAGCAGCAGA 588  
QY 552 TGGCTGAGAGCAAGGCTCTGTGAAAGCCAGGTGACGTCTTGTCTCGGGAGCTGACAG 611  
DB 589 TGGCTGAGAGCAAGGCTCTGTGAAAGCCAGGTGACGTCTTGTCTCGGGAGCTGACAG 648  
QY 612 AGAGCAGAGTCTGTTGGAGGCTGCACTTAAGGAATGCCAGGCTCTGGAAGGTTGGGGCC 671  
DB 649 AGAGCAGAGTCTGTTGGAGGCTGCACTTAAGGAATGCCAGGCTCTGGAAGGTTGGGGCC 708  
QY 672 GGGCGCCAGCAGAGCAGCGCGCAGCTGGAGTGGAGCGCGAGGCGCTGCGAGCAGCAGC 731  
DB 709 GGGCGCCAGCAGAGCAGCGCGCAGCTGGAGTGGAGCGCGAGGCGCTGCGAGCAGCAGC 768  
QY 732 ACAGCTGTCAGTGTGACAGCTGCGCATGCGAGGCGCAGAGCGTGGAGGCGCGCTCCGCA 791  
DB 769 ACAGCTGTCAGTGTGACAGCTGCGCATGCGAGGCGCAGAGCGTGGAGGCGCGCTCCGCA 828  
QY 792 TGGAGCGCCAGCGCCCTCGGAGGAGAGAGAACTGGCCCACTTGCAGGTGGCCCTATC 851  
DB 829 TGGAGCGCCAGCGCCCTCGGAGGAGAGAGAACTGGCCCACTTGCAGGTGGCCCTATC 888  
QY 852 ACCAGCTCTTCCAAGAAATACGACAAACCATCAAGAGCAGCGTGGTGGGAGCGAGCGGA 911  
DB 889 ACCAGCTCTTCCAAGAAATACGACAAACCATCAAGAGCAGCGTGGTGGGAGCGAGCGGA 948  
QY 912 AGCGAGGAATGAGCTGGAAGATCTCAAACAGCAGCTCCAGCAGGCGCGAGGAGCGCCCTGG 971  
DB 949 AGCGAGGAATGAGCTGGAAGATCTCAAACAGCAGCTCCAGCAGGCGCGAGGAGCGCCCTGG 1008  
QY 972 TGGCCCAAACAGGAGTGTGATAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1031  
DB 1009 TGGCCCAAACAGGAGTGTGATAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1068  
QY 1032 TGGAGACCGTTCCGGTGTCTGAAGGCGCCAGGCGGATATCTTACAAGGCGGACTTCCAGGCTG 1091  
DB 1069 TGGAGACCGTTCCGGTGTCTGAAGGCGCCAGGCGGATATCTTACAAGGCGGACTTCCAGGCTG 1128  
QY 1092 AGAGCAGCGCCCGGAGAGCTGGCCGAGAGAGAGAGAGTCTCTGAGAGAGCAGCTGGAGC 1151  
DB 1129 AGAGCAGCGCCCGGAGAGCTGGCCGAGAGAGAGAGAGTCTCTGAGAGAGCAGCTGGAGC 1188  
QY 1152 AGCTGAGAGGAGTACAGCAAACTGAAGGCGCAGCTGTGAGAGTGGCCAGGATCGAGG 1211  
DB 1189 AGCTGAGAGGAGTACAGCAAACTGAAGGCGCAGCTGTGAGAGTGGCCAGGATCGAGG 1248  
QY 1212 ACATGAGGAAGCGGATGTGAGAGTCTCCAGGCGCCCTTGGCCCGCCCTCGCTTACC 1271  
DB 1249 ACATGAGGAAGCGGATGTGAGAGTCTCCAGGCGCCCTTGGCCCGCCCTCGCTTACC 1308  
QY 1272 TCTCTCTCTCCCTGCGCTGCGCCAGCAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1331  
DB 1309 TCTCTCTCTCCCTGCGCTGCGCCAGCAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1368  
QY 1332 TCTGTCTCTCCAAAGTGCAGTATCAGGCGCCCTGATATGAGACACCTTGCAGATACATGTCA 1391  
DB 1369 TCTGTCTCTCCAAAGTGCAGTATCAGGCGCCCTGATATGAGACACCTTGCAGATACATGTCA 1428  
QY 1392 TGGAGTGCATTTAGTGGGCGCGCAGTGCAGAGGCACTTGCCTGCGCGGAGGAGGAGGAGGAGG 1451  
DB 1429 TGGAGTGCATTTAGTGGGCGCGCAGTGCAGAGGCACTTGCCTG-CCGAGGAGGAGGAGGAGG 1487  
QY 1452 GAGCGTGCAGTGTGCGCTTTCCTCTCCGCGCTGCTAGCCAGGATGAAGGAGGAGGAGGAGGAGG 1511  
DB 1488 GAGCGTGCAGTGTGCGCTTTCCTCTCCGCGCTGCTAGCCAGGATGAAGGAGGAGGAGGAGGAGG 1547



QY 1451 GGGACCGTGCAGTCTGGCTTTCTCTCCCGCTGCTAGCCAGGATGAAGGCTGGGT 1510  
Db 1412 GGGACCGTGCAGTCTGGCTTTCTCTCCCGCTGCTAGCCAGGATGAAGGCTGGGT 1471  
QY 1511 GGGACAACTGGGATGCCACTGGAGGCCACCCAGGAGTGGCCGGGCACTTACGCT 1570  
Db 1472 GGGACAACTGGGATGCCACTGGAGGCCACCCAGGAGTGGCCGGGCACTTACGCT 1531  
QY 1571 TCAGCTGTTGATCCGCTGGTCCCTCTTTTGGGTAGATCGGCCCCGATCAGGCTGAC 1630  
Db 1532 TCAGCTGTTGATCCGCTGGTCCCTCTTTTGGGTAGATCGGCCCCGATCAGGCTGAC 1591  
QY 1631 TCCTGCTCTTTTGTTCCTCTCTGCTCGAACCACTTGGCTCGGGCTAATCCCTCC 1690  
Db 1592 TCCTGCTCTTTTGTTCCTCTCTGCTCGAACCACTTGGCTCGGGCTAATCCCTCC 1651  
QY 1691 CTCCTTCCACCCGCACTGGGGAGTCAAGAAATGGGCTCTCAGGGAGAAC 1750  
Db 1652 CTCCTTCCACCCGCACTGGGGAGTCAAGAAATGGGCTCTCAGGGAGAAC 1711  
QY 1751 TGCTTCCCTGGCAGAGTGGGTGGAGCTCTTCTCCACCGGACACCGGCCCGCC 1810  
Db 1712 TGCTTCCCTGGCAGAGTGGGTGGAGCTCTTCTCCACCGGACACCGGCCCGCC 1771  
QY 1811 CGCTGTCCTGGGAGTGTGCTCTTACCATGACACGGGTGCTCTCTTTTGGGCTG 1870  
Db 1772 CGCTGTCCTGGGAGTGTGCTCTTACCATGACACGGGTGCTCTCTTTTGGGCTG 1831  
QY 1871 CATGCTATTCCATTTTGCAGCCAGACCGATGTATTTAACAGTCACTATTGATGGACA 1930  
Db 1832 CATGCTATTCCATTTTGCAGCCAGACCGATGTATTTAACAGTCACTATTGATGGACA 1891  
QY 1931 TTTGGGTGTGTTCCCATCTTTTGTACCATAAATATGTCATAGTAAAAA 1981  
Db 1892 TTTGGGTGTGTTCCCATCTTTTGTACCATAAATATGTCATAGTAAAAA 1942

RESULT 6  
US-10-628-841-10  
; Sequence 10, Application US/10628841  
; Publication No. US20040023918A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-GAMMA EXPRESSION  
; FILE REFERENCE: RTS-0191  
; CURRENT APPLICATION NUMBER: US/10/628,841  
; CURRENT FILING DATE: 2003-07-28  
; PRIOR APPLICATION NUMBER: US/09/972,607  
; PRIOR FILING DATE: 2001-10-06  
; NUMBER OF SEQ ID NOS: 88  
; SEQ ID NO 10  
; LENGTH: 1975  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (111)...(1370)  
US-10-628-841-10

Query Match 91.9%; Score 1832.6; DB 17; Length 1975;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1846; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 131 CAGCCCTTCCCTGTGGATGAATAGGCACTCTGGAAGAGCCAACTGTGTGAGATGGTG 190  
Db 93 CAGCCCTTCCCTGTGGATGAATAGGCACTCTGGAAGAGCCAACTGTGTGAGATGGTG 152  
QY 191 CAGCCAGTGTGGCCCGCAGCAGATCAGGACGTCTGGCGGAGAGTCTCTCTGGGG 250  
Db 153 CAGCCAGTGTGGCCCGCAGCAGATCAGGACGTCTGGCGGAGAGTCTCTCTGGGG 212  
QY 251 AAGCCAGCCATGTGCACCTGCTTTCAGAAAGGGCGCTCCTGAGACCCCTCCAGCGCTGC 310

Db 213 AAGCCAGCCATGTGCACCTGCTTTCAGAAAGGGCGCTCCTGAGACCCCTCCAGCGCTGC 272  
QY 311 CTGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACAGATTTTCGGGAG 370  
Db 273 CTGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACAGATTTTCGGGAG 332  
QY 371 CGCTGCGAGGAGCTTCTGCATTTTCCAAAGCCAGCAGAGGAGGAGAGGATTCCTCATG 430  
Db 333 CGCTGCGAGGAGCTTCTGCATTTTCCAAAGCCAGCAGAGGAGGAGAGGATTCCTCATG 392  
QY 431 TGCAAAGTTCCAGAGGCCAGGAACTGTGTGGAGAGACTCGGCCCTGGAGAACTCGATCTG 490  
Db 393 TGCAAAGTTCCAGAGGCCAGGAACTGTGTGGAGAGACTCGGCCCTGGAGAACTCGATCTG 452  
QY 491 AAGAGCACAAGGAGCAGAGCTCTGCGGAGGTGGAGCACTGGAAGATGCCAGAGCAG 550  
Db 453 AAGAGCACAAGGAGCAGAGCTCTGCGGAGGTGGAGCACTGGAAGATGCCAGAGCAG 512  
QY 551 ATGGCTGAGGACAAGGCCCTCTGTGAAGCCAGGTGACGTCTTGTCTCGGGAGGCTGCAG 610  
Db 513 ATGGCTGAGGACAAGGCCCTCTGTGAAGCCAGGTGACGTCTTGTCTCGGGAGGCTGCAG 572  
QY 611 GAGAGCCAGAGTCCGCTTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGAGAGGTCCGGCC 670  
Db 573 GAGAGCCAGAGTCCGCTTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGAGAGGTCCGGCC 632  
QY 671 CGGGCGCCAGCAGCAGCGCGGAGCTGGAGAGTGGAGCGGAGCGCTGTCAGAGCAG 730  
Db 633 CGGGCGCCAGCAGCAGCGCGGAGCTGGAGAGTGGAGCGGAGCGCTGTCAGAGCAG 692  
QY 731 CACAGGTGCAGTGGAGCAGCTGCGCATGCAAGGGCCAGAGCTGTCAGAGCGCGCTCCGC 790  
Db 693 CACAGGTGCAGTGGAGCAGCTGCGCATGCAAGGGCCAGAGCTGTCAGAGCGCGCTCCGC 752  
QY 791 ATGGAGCGCCAGCGCCCTCTCGAGGAGAAAGAGAACTGCGCCAGTTGTCAGAGTGGCTAT 850  
Db 753 ATGGAGCGCCAGCGCCCTCTCGAGGAGAAAGAGAACTGCGCCAGTTGTCAGAGTGGCTAT 812  
QY 851 CACAGCTCTTCCAGAGATACCAACCAATCAAGAGCAGCGTGTGGGAGTGAAGCGG 910  
Db 813 CACAGCTCTTCCAGAGATACCAACCAATCAAGAGCAGCGTGTGGGAGTGAAGCGG 872  
QY 911 AAGCCAGGAATCAGCTGGAAGATCTCAACAGCAGCTCCAGCAGGCCCGAGAGGCCCTG 970  
Db 873 AAGCCAGGAATCAGCTGGAAGATCTCAACAGCAGCTCCAGCAGGCCCGAGAGGCCCTG 932  
QY 971 GTGGCCAAAACAGGAGGTGATTCGATAAGCTGAAGGAGGAGCGGAGCAGCAAGATTGTG 1030  
Db 933 GTGGCCAAAACAGGAGGTGATTCGATAAGCTGAAGGAGGAGCGGAGCAGCAAGATTGTG 992  
QY 1031 ATGGAGACCGTTTCCGCTGCTGAAGGCCCAAGCGGATATCTCAAGCGCACTTCCAGGCT 1090  
Db 993 ATGGAGACCGTTTCCGCTGCTGAAGGCCCAAGCGGATATCTCAAGCGCACTTCCAGGCT 1052  
QY 1091 GAGAGCGAGCCCGGAGAGAGCTGGCCGAGAGAGAGGAGCTCTTCGAGAGCAGCTGGAG 1150  
Db 1053 GAGAGCGAGCCCGGAGAGAGCTGGCCGAGAGAGAGGAGCTCTTCGAGAGCAGCTGGAG 1112  
QY 1151 CAGCTGTCAGAGGAGGTACAGCAAACTGAAGGGCCAGCTGTGAGAGTTCGGCCAGGATCCGAG 1210  
Db 1113 CAGCTGTCAGAGGAGGTACAGCAAACTGAAGGGCCAGCTGTGAGAGTTCGGCCAGGATCCGAG 1172  
QY 1211 GACATGAGAGAGCGGATGTTCAGGTCTCCAGGCCCTTCGCCGCCCTTCGCTTAC 1270  
Db 1173 GACATGAGAGAGCGGATGTTCAGGTCTCCAGGCCCTTCGCCGCCCTTCGCTTAC 1232  
QY 1271 CTCCTCTCTCCCTGGCCCTGCCAGCAGAGGAGGAGCCCCCGAGAGGAGCCACTGAC 1330  
Db 1233 CTCCTCTCTCTCCCTGGCCCTGCCAGTCAAGAGAGGAGGAGCCCCCGAGAGGAGCCACTGAC 1292  
QY 1331 TTTCTCTCTCTCCCAAGTGGCCAGTATCAGGCCCTGTATGGAACCTCTGAGACCTCTGAGATATGTC 1390



Db 1293 TTCTGCTGCCAAGTCCAGTATCAGGCCCTGATATGACACCCCTGCAGATACATGTC 1352  
Qy 1391 ATGAGTGCATAGTAGGCGCGGCGAGTGCAGGCCACTGCTGCGCCGAGGACGTGCC 1450  
Db 1353 ATGAGTGCATAGTAGGCGCGGCGAGTGCAGGCCACTGCTG-CGAGGACGTGCC 1411  
Qy 1451 GAGACCGTGCAGTCCGCTTTCCTCTCCGCGCTGCTAGGCCAGAGTGAAGGCTGGT 1510  
Db 1412 GAGACCGTGCAGTCCGCTTTCCTCTCCGCGCTGCTAGGCCAGAGTGAAGGCTGGT 1471  
Qy 1511 GGCACAACTGGGATGCCACTGGAGCCCAACCCAGGAGTGGCCGCGGCACTTACGCT 1570  
Db 1472 GGCACAACTGGGATGCCACTGGAGCCCAACCCAGGAGTGGCCGCGGCACTTACGCT 1531  
Qy 1571 TCAGCTGTTGATCCGCTGGTCCCTCTTTTGGGTAGATGCGGCCCGCATCAGGCTGAC 1630  
Db 1532 TCAGCTGTTGATCCGCTGGTCCCTCTTTTGGGTAGATGCGGCCCGCATCAGGCTGAC 1591  
Qy 1631 TCCTGCTCTTTTGTTCCTCTGCTGCTCGAACCACTTGCCTCGGCTGCTGCTCCCTCC 1690  
Db 1592 TCCTGCTCTTTTGTTCCTCTGCTGCTCGAACCACTTGCCTCGGCTGCTGCTCCCTCC 1651  
Qy 1691 CTCTTCTCCACCCGCACTGGGGAGTCAAGAAATGGGGCTCTCAGGGAGAAC 1750  
Db 1652 CTCTTCTCCACCCGCACTGGGGAGTCAAGAAATGGGGCTCTCAGGGAGAAC 1711  
Qy 1751 TGCTTCCCTGGCAGAGCTGGTGGGAGTCTTCTCCGCGGACACCGACCGCCCGC 1810  
Db 1712 TGCTTCCCTGGCAGAGCTGGTGGGAGTCTTCTCCGCGGACACCGACCGCCCGC 1771  
Qy 1811 CGCTGTCCTGGGAGTGTGCTCTTACCATGCACACGGGTGTCTCTCTTTTGGGTG 1870  
Db 1772 CGCTGTCCTGGGAGTGTGCTCTTACCATGCACACGGGTGTCTCTCTTTTGGGTG 1831  
Qy 1871 CATGCTATTCATTTTGCAGCAGACCGAGTGTATTAACACAGTCACTATTGATGACA 1930  
Db 1832 CATGCTATTCATTTTGCAGCAGACCGAGTGTATTAACACAGTCACTATTGATGACA 1891  
Qy 1931 TTTGGGTGTTTCCCATCTTTTGTACCATAAATAGGCATAGTAAAA 1981  
Db 1892 TTTGGGTGTTTCCCATCTTTTGTACCATAAATAGGCATAGTAAAA 1942

## RESULT 7

US-10-761-370-1  
; Sequence 1, Application US/10761370  
; Publication No. US20040219615A1  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR  
; FILE REFERENCE: WALLACH-27  
; CURRENT APPLICATION NUMBER: US/10/761,370  
; CURRENT FILING DATE: 2004-01-22  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR FILING DATE: 1999-03-18  
; PRIOR FILING DATE: 1999-03-18  
; PRIOR FILING DATE: 1998-09-01  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2009  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-761-370-1

Query Match 91.4%; Score 1823; DB 18; Length 2009;  
Best Local Similarity 99.6%; Pred. No. 0;

Matches 1845; Conservative 3; Mismatches 3; Indels 2; Gaps 2;  
Qy 131 CAGCCCTTGCCTCTTGATGAATAGGCACCTCTTGAAGAGCCAACTGTGTGAGATGGT 190  
Db 136 CAGCCCTTGCCTCTTGATGAATAGGCACCTCTTGAAGAGCCAACTGTGTGAGATGGT 195  
Qy 191 CAGCCCTTGCCTCTTGATGAATAGGCACCTCTTGAAGAGCCAACTGTGTGAGATGGT 250  
Db 196 CAGCCCTTGCCTCTTGATGAATAGGCACCTCTTGAAGAGCCAACTGTGTGAGATGGT 255  
Qy 251 AAGCCAGCATGCTGACCTTCCAGAACAGAGCGCTCTGAGACCTCCAGCGCTGC 310  
Db 256 AAGCCAGCATGCTGACCTTCCAGAACAGAGCGCTCTGAGACCTCCAGCGCTGC 315  
Qy 311 CTGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACACAGATTCTCGGGAG 370  
Db 316 CTGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACACAGATTCTCGGGAG 375  
Qy 371 CGCTGCCAGGAGCTTCTGCATTTCCAAAGCCAGACAGAGGAGGAGAGGATTCCTCATG 430  
Db 376 CGCTGCCAGGAGCTTCTGCATTTCCAAAGCCAGACAGAGGAGGAGAGGATTCCTCATG 435  
Qy 431 TGCAAGTTTCAGAGGAGCCAGGAACTCGTGGAGAGACTCGGCCTGGAGAGCTCGATCTG 490  
Db 436 TGCAAGTTTCAGAGGAGCCAGGAACTCGTGGAGAGACTCGGCCTGGAGAGCTCGATCTG 495  
Qy 491 AAGAGCAGAAAGAGCAGGCTCTGCGGAGGTGGAGCACTTGAAGAGATGCCAGCAG 550  
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Qy 551 ATGCTCAGACAGAGGCTCTGTAAGCCAGCTGAGCTCTTCTCGGGAGGAGTGCAG 610  
Db 556 ATGCTCAGACAGAGGCTCTGTAAGCCAGCTGAGCTCTTCTCGGGAGGAGTGCAG 615  
Qy 611 GAGAGCCAGAGTCCGCTTGGAGGCTGCCACTAAGAAATGCCAGGCTCTGAGGGTCCGGCC 670  
Db 616 GAGAGCCAGAGTCCGCTTGGAGGCTGCCACTAAGAAATGCCAGGCTCTGAGGGTCCGGCC 675  
Qy 671 CGGCGGCCAGCAGCAGCGCGGCTGAGAGTGAAGAGGAGGCTCAGCAGCAG 730  
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Qy 731 CACAGCGTCAGGTGGACACAGCTGCGATGCGAGGCGCAGAGCTGGAGGCGCTCCGC 790  
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Qy 851 CACAGCTCTTCAAGAAATACGACCAACATCAAGAGCAGCTGGTGGGAGTGGAGCGG 910  
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Qy 911 AAGCGAGAAATGAGTGGAGATCTCAAAACAGCAGCTCCAGAGGCGCGAGAGGCGCTG 970  
Db 916 AAGCGAGAAATGAGTGGAGATCTCAAAACAGCAGCTCCAGAGGCGCGAGAGGCGCTG 975  
Qy 971 GTGGCCAAACAGAGGTGATCGATAAGCTGAAAGAGGAGGCGGAGCAGCAAGATTGTG 1030  
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Qy 1031 ATGAGAGCTTCCGCTGCTGAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1090  
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Qy 1091 GAGAGCAGCGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1150  
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Qy 1151 CAGCTCAGAGGAGTACAGCAACTGAAGGCCAGGCTGTGAGGAGTCCGCCAGGATCGAG 1210  
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Qy	1211	GACATGAGGAAGCGGCATGTGAGGTTCTCCAGGCGCCCTTGGCCCCCGCCCTGTCCTAC	1270
Db	1216	GACATGAGGAAGCGGCATGTGAGGTTCTCCAGGCGCCCTTGGCCCCCGCCCTGTCCTAC	1275
	1271	CTCTCTCTCCCTTGGCCCTGCCAGACGAGGAGGAGCCCCCGGAGGAGCCACCTGAC	1330
Db	1276	CTCTCTCTCCCTTGGCCCTGCCAGCGAGGAGGAGCCCCCGGAGGAGCCACCTGAC	1335
Qy	1331	TTCTGCTGTCCCAAGTGCAGTATCAGGCCCCCTGATATGGACACCCCTGCAGATACATGTC	1390
Db	1336	TTCTGCTGTCCCAAGTGCAGTATCAGGCCCCCTGATATGGACACCCCTGCAGATACATGTC	1395
Qy	1391	ATGAGATGCATTTGATGAGGCGGCCAGTGCAGGCCACTGCTCTGCGCCGAGGACGTGCCCC	1450
Db	1396	ATGAGATGCATTTGATGAGGCGGCCAGTGCAGGCCACTGCTCTGCGCCGAGGACGTGCCCC	1454
Qy	1451	GGGACCGTGCAAGTCTGCGCTTCTCTCTCGCGCTGCTCTAGCCACAGATGAAGGGCTGGGT	1510
Db	1455	GGGACCGTGCAAGTCTGCGCTTCTCTCTCGCGCTGCTCTAGCCACAGATGAAGGGCTGGGT	1514
Qy	1511	GGCCACAACCTGGGATGCCACTGAGAGCCCAACCCAGGAGCTGGCGCGGCACCTTAAGCT	1570
Db	1515	GGCCACAACCTGGGATGCCACTGAGAGCCCAACCCAGGAGCTGGCGCGGCACCTTAAGCT	1574
Qy	1571	TCAGCTGTGGA-TCCGCTGGTCCCTCTTTTGGGGTAGATGCGGCCCGCATCAGGCGCTGA	1629
Db	1575	TCAGCTGTGGA-TCCGCTGGTCCCTCTTTTGGGGTAGATGCGGCCCGCATCAGGCGCTGA	1634
Qy	1630	CTCGCTCTCTTTTGTTCCTTCTGTCTGTCTCGAACCACTTGGCTCGGGCTTAATCCCTC	1689
Db	1635	CTCGCTCTCTTTTGTTCCTTCTGTCTGTCTCGAACCACTTGGCTCGGGCTTAATCCCTC	1694
Qy	1690	CTCTTCTCTCGACCCGGGCACTGGGGAAGTCAAGAAATGGGGCTTGGGGCTCTCAGGAGAA	1749
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Qy	1750	CTGCTTCCCTTGGCAGAGCTGGGTGGCAGCTCTTCTCCACCCGGACACCGACCCGCCCG	1809
Db	1755	CTGCTTCCCTTGGCAGAGCTGGGTGGCAGCTCTTCTCCACCCGGACACCGACCCGCCCG	1814
Qy	1810	CCGCTGTGCCCTGGGAGTGTGCCCTCTTACCATGCACACGGGTGCTCTCTTTTGGGCT	1869
Db	1815	CTGCTGTGCCCTGGGAGTGTGCCCTCTTACCATGCACACGGGTGCTCTCTTTTGGGCT	1874
Qy	1870	GCAATGCTAATTTCCATTTTTCAGCCAGACCGATGTGTATTTTAAACCAAGTCACCTAATGATGGAC	1929
Db	1875	GCAATGCTAATTTCCATTTTTCAGCCAGACCGATGTGTATTTTAAACCAAGTCACCTAATGATGGAC	1934
Qy	1930	ATTTGGGTTGTTTCCCATCTTTTGTGTACATAAATATGGCATAGTAAAAA	1982
Db	1935	ATTTGGGTTGTTTCCCATCTTTTGTGTACATAAATATGGCATAGTAAAAA	1987

RESULT 8  
US-10-761-370-2  
; Sequence 2, Application US/10761370  
; Publication No. US20040219615A1  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: KOVALENKO, Andrei  
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR F  
; TITLE OF INVENTION: AND OTHER PROTEINS  
; FILE REFERENCE: WALLACH=27  
; CURRENT APPLICATION NUMBER: US/10/761.370  
; CURRENT FILING DATE: 2004-01-22  
; PRIOR APPLICATION NUMBER: US/09/646,403  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: IL 123758  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: PCT/IL99/00158  
; PRIOR FILING DATE: 1999-03-18  
; PRIOR APPLICATION NUMBER: IL 126024

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; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2034
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-761-370-2

Query Match      88.1%; Score 1757.2; DB 18; Length 2034;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 1826; Conservative 3; Mismatches 21; Indels 8; Gaps 5;

Qy 132 AGCCCTTGCCCTCTTGATGAATAGGACCTCTGGAAGAGCCAACTGTGTGAGATGGTGC 191
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Qy 192 AGCCCAAGTGTGTGCCCGGACAGAGATCAGAGACGTACTGGCGGAAGAGTCTCCCTCTGGGA 251
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Db 215 AGCCCAAGTGTGTGCCCGGACAGAGATCAGAGACGTACTGGCGGAAGAGTCTCCCTCTGGGA 274
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Qy 252 AGCCAGCCATGTCTGCACCTGCCCTTCAGAAACAGGGCGCTCTCTGAGACCCTCCAGCGCTGCC 311
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Qy 312 T-CGAGGAGNATCAAGAGCTCCGAGATGCGATCCGGCAG-AGCAACACAGATTCTCGGGGA 369
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Db 335 TGGGAGGAGNATCAAGAGCTCCGAGATGCGATCCGGCAGTAGCAACACAGATTCTTCGGGG 394
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Qy 370 GCGCTCGAGGAGCTTCTGC-----ATTTCACAGCCAGGAGGAGGAGAGAGTTC 425
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Qy 426 TCATGTGCAAGTTCACGAGGCGCAGGAAACTGCTGGAGAGACTCGGCCTGGAGAACTCG 485
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Qy 666 GGGCCCGGGCGGCCAGGAGCAGGCGCGCAGCTGAGAGTGTAGCGGAGGCGCTGCAGC 725
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Db 695 GGGCCCGGGCGGCCAGGAGCAGGCGCGCAGCTGAGAGTGTAGCGGAGGCGCTGCAGC 754
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Qy 726 AGCAGACACAGCTGCAAGTGGACCAAGCTCGCATGCAGGCGCAGAGCGTGGAGGCGCGCG 785
    |||
Db 755 AGCAGACACAGCTGCAAGTGGAGTGGACCAAGCTCGCATGCAGGCGCAGAGCGTGGAGGCGCGCG 814
    |||

Qy 786 TCCGCATGAGAGCGCCAGGCGCGCTCGGAGGAGAAAGAGTGTGGCCCAAGTTGCAGGTGG 845
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Db 815 TCCGCATGAGAGCGCCAGGCGCGCTCGGAGGAGAAAGAGTGTGGCCCAAGTTGCAGGTGG 874
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Qy 846 CCTATCACCAAGCTCTTCCAAAGATACGACAAACACATCAAGAGCAGCGTGTGGGAGTGG 905
    |||
Db 875 CCTATCACCAAGCTCTTCCAAAGATACGACAAACACATCAAGAGCAGCGTGTGGGAGTGG 934
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Qy 906 AGCGGAAGCGGGAATGCAAGCTGGAGATCTCAACAGCAGCTCTCCAGCAGGCGCGAGGAGG 965
    |||
Db 935 AGCGGAAGCGGGAATGCAAGCTGGAGATCTCAACAGCAGCTCTCCAGCAGGCGCGAGGAGG 994
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Qy 966 CCCTGTGTCGCAAAACAGGAGGTGATCGATAAGCTGAAGGAGGAGGCGCGAGCACAAGA 1025
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Db 995 CCCTGTGTCGCAAAACAGGAGGTGATCGATAAGCTGAAGGAGGAGGCGCGAGCACAAGA 1054
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; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-792-063-6

Query Match      20.2%; Score 402.6; DB 18; Length 483;
Best Local Similarity 99.0%; Pred. No. 3.1e-98;
Matches 405; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 149 ATGAATAGGCACCTCTGGAAGAGCCAACTGTGTGAGATGGTGACCCAGTGGTGGCCCG 208
Db 1 ATGAATAGGCACCTCTGGAAGAGCCAACTGTGTGAGATGGTGACCCAGTGGTGGCCCG 60

Qy 209 GCAGCAGATCAGGACGTAATCTGGCGGAAGAGTCTCTCTGGGGAAGCCAGCCATGTGCAC 268
Db 61 GCAGCAGATCAGGACGTAATCTGGCGGAAGAGTCTCTCTGGGGAAGCCAGCCATGTGCAC 120

Qy 269 CTGCTTTCAGAACAGGCGCTCTGAGACCTCCAGACCTGCTGGAGGAGAAATCAAGAG 328
Db 121 CTGCTTTCAGAACAGGCGCTCTGAGACCTCCAGACCTGCTGGAGGAGAAATCAAGAG 180

Qy 329 CTCGAGATGCCATCCGGCAGAGCAACCAAGATTCTGCGGGAGCGCTGCGAGAGCTTCTG 388
Db 181 CTCGAGATGCCATCCGGCAGAGCAACCAAGATTCTGCGGGAGCGCTGCGAGAGCTTCTG 240

Qy 389 CATTTCCAGCCAGCCAGAGGAGAGAGAGTTCCTCATGTGCAAGTTCAGGAGGCC 448
Db 241 CATTTCCAGCCAGCCAGAGGAGAGAGAGTTCCTCATGTGCAAGTTCAGGAGGCC 300

Qy 449 AGGAAACTGGTGGAGAGACTCGGCTGGAGAGCTCGATCTGAAGAGGCCAAGAGGAG 508
Db 301 AGGAAACTGGTGGAGAGACTCGGCTGGAGAGCTCGATCTGAAGAGGCCAAGAGGAG 360

Qy 509 GCTCTGCGGGAGGTGGAGCACCCTGAAGAGATGCCAGCAGCAGATGGCTG 557
Db 361 GCTCTGCGGGAGGTGGAGCACCCTGAAGAGATGCCAGCAGCAGATGGCTG 409
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## RESULT 15

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US-09-925-298-84/c
; Sequence 84, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 2803
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (50)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (517)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (572)
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; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1926)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-298-84
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Query Match      13.9%; Score 277.6; DB 9; Length 2803;
Best Local Similarity 95.2%; Pred. No. 3.1e-64;
Matches 280; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 131 CAGCCCTTGCCCTGTTGGATGAATAGGCACCTCTGGAAGAGCCCACTGTGTGAGATGGTG 190
Db 302 CAGCCCTTGCCCTGTTGGATGAATAGGCACCTCTGGAAGAGCCCACTGTGTGAGATGGTG 243

Qy 191 CAGCCCAAGTGGTGGCCCGGAGCAGATCAGGACCTACTGGGCGGAAGAGTCTCTCTGGGG 250
Db 242 CAGCCCAAGTGGTGGCCCGGAGCAGATCAGGACCTACTGGGCGGAAGAGTCTCTCTGGGG 183

Qy 251 AAGCCAGCCATGTGTGACCTGCTTTCAGAACAGGGCGCTCTGAGACCTCCAGCGCTGC 310
Db 182 AAGCCAGCCATGTGTGACCTGCTTTCAGAACAGGGCGCTCTGAGACCTCCAGCGCTGC 123

Qy 311 CTGAGGAGAGATCAAGAGCTCCGAGATGCCATCCGCGAGACCAACCAGATTCTGCGGGAG 370
Db 122 CTGAGGAGAGATCAAGAGCTCCGAGATGCCATCCGCGAGACCAACCAGATTCTGCGGGAG 63

Qy 371 CGCTGCGAGAGCTTCTGCAATTTCCAAAGCCAGCCAGAGGGAGGAGAGGAGTTTC 424
Db 62 CGTTGCGAGAGNTTTTGSATTTTCCAAAGCCAGCCAGAGGGAGGAGAGGAGTTTC 9
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Search completed: February 9, 2005, 03:17:38  
Job time : 1093 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 8, 2005, 21:27:04 ; Search time 6675 Seconds  
(without alignments)  
11370.809 Million cell updates/sec

Title: US-09-377-795-1

Perfect score: 1994

Sequence: 1 ggcagcagcatggcccttgt.....gtataaaaaaa 1994

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gssi:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1850.4	92.8	1960	3	BC046922 Homo sapi
2	1820.4	91.3	1958	3	CR600010 full-leng
3	1816.8	91.1	1962	6	CA916723 K142FL hu
4	1794.4	90.0	1943	3	CR604149
5	1466.4	73.5	1751	3	CR603029 full-leng
6	1151.4	57.7	1164	3	CR612085 full-leng
C 7	997.4	50.0	1039	1	AL575675
C 8	948	47.5	1115	1	AL582339
C 9	927.6	46.5	4335	3	AK037020 Mus muscu
C 10	916.8	46.0	1081	1	AL568758
C 11	914.2	45.8	1036	5	EX325315
C 12	880.2	44.1	1118	5	EX332283
C 13	877.6	44.0	908	5	BQ674261
C 14	866.6	43.5	913	1	AL572134
C 15	859.2	43.1	935	1	AL580495
C 16	850	42.6	888	1	AL521144
C 17	834.2	41.8	1016	5	EX361771
C 18	828.8	41.6	879	5	EX331837
C 19	824.8	41.4	925	5	EX328265
C 20	822.2	41.2	1043	1	AL541141
C 21	818.8	41.1	974	1	AL545822
C 22	813.6	40.8	878	5	BU197200
C 23	813	40.8	875	1	AL558739
C 24	809.8	40.6	975	5	EX418245

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26	778.8	39.1	1011	5	EX325316	EX325316	AGENCOURT
27	778.8	39.1	1098	4	BM473416	BM473416	AGENCOURT
28	774.8	38.9	957	5	BQ932422	BQ932422	AGENCOURT
29	765	38.4	1024	1	AL558226	AL558226	AGENCOURT
30	764	38.3	1098	4	BM478785	BM478785	AGENCOURT
C 31	762.2	38.2	974	1	AL562815	AL562815	AGENCOURT
C 32	761	38.2	919	1	AL547021	AL547021	AGENCOURT
C 33	754.6	37.8	920	5	EX418246	EX418246	AGENCOURT
C 34	742.6	37.2	858	1	AL571390	AL571390	AGENCOURT
C 35	739.8	37.1	902	5	BQ944161	BQ944161	AGENCOURT
C 36	738.4	37.0	872	5	EX418606	EX418606	AGENCOURT
C 37	732.6	36.7	865	5	BU170415	BU170415	AGENCOURT
C 38	712.6	35.7	1091	4	BM467195	BM467195	AGENCOURT
C 39	702	35.2	877	5	EX434638	EX434638	AGENCOURT
C 40	697.8	35.0	931	5	BU154734	BU154734	AGENCOURT
C 41	693.4	34.8	707	5	BU616100	BU616100	AGENCOURT
C 42	688.4	34.5	701	5	BU626925	BU626925	AGENCOURT
C 43	688.4	34.5	701	5	BU633401	BU633401	AGENCOURT
C 44	685.6	34.4	929	5	BU528711	BU528711	AGENCOURT
C 45	683.6	34.3	708	5	BU615463	BU615463	AGENCOURT

## ALIGNMENTS

BC046922	1960 bp	mRNA	linear	HTC 19-NOV-2003
Homo sapiens	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma, mRNA (cdna clone IMAGE:5476394), containing frame-shift errors.			
BC046922	GI:28422142			
HTC				
Homo sapiens	(human)			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
1 (bases 1 to 1960)				
Strasbourg, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.				
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
22388257				
12477932				
2 (bases 1 to 1960)				
Strasbourg, R.				
Direct Submission				
Submitted (14-FEB-2003)				
National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>				
Contact: MGC help desk				
Email: <a href="mailto:cgabbs@mail.nih.gov">cgabbs@mail.nih.gov</a>				





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QY 1331 TTCTGCTGTCCTCCAGTGCAGTATCAGGCCCTGTATGACACACCTGTCAGATACATGTC 1390
Db 1326 TTCTGCTGTCCTCCAGTGCAGTATCAGGCCCTGTATGACACACCTGTCAGATACATGTC 1385
QY 1391 ATGAGTGCATTGAGTAGGCGCGGCGAGTGCAGGCCACTGTGCTGCCCGAGGACGTGCC 1450
Db 1386 ATGAGTGCATTGAGTAGGCGCGGCGAGTGCAGGCCACTGTGCTGCCCGAGGACGTGCC 1444
QY 1451 GGGACCGTGCAGTCTGGGCTTTCTCTCCGCGCTGCTAGCCAGAGTGAAGGCTGGGT 1510
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QY 1811 CGCTGCGCTGGAGTGTGCTCTTACCATGACACAGGGTGTCTCTTTGGGCTG 1870
Db 1805 TGCTGCGCTGGAGTGTGCTCTTACCATGACACAGGGTGTCTCTTTGGGCTG 1864
QY 1871 CATGCTATTTCATTTTGCAGCAGACCGATGTTATTTAAACAGTCACTATTGATGGACA 1930
Db 1865 CATGCTATTTCATTTTGCAGCAGACCGATGTTATTTAAACAGTCACTATTGATGGACA 1924
QY 1931 TTTGGGTTGTTCCCATCTTTTGTACATAAA 1964
Db 1925 TTTGGGTTGTTCCCATCTTTTGTACATAAA 1958

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RESULT 3
CA916723
LOCUS
DEFINITION
  CA916723 human keratinocyte matchmaker cDNA library Homo sapiens cDNA
  clone K142 5' similar to IKK gamma/ NEMO, mRNA sequence.
ACCESSION
  CA916723
VERSION
  CA916723.1 GI:28951960
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 1962)
  Scarafia, L.E., Stouffer, S.D. and Swinney, D.C.
  Identification of Ring Finger proteins that interact with Ubch5a,
  an ubiquitin-conjugating enzyme
  Unpublished (2002)
  Contact: Scarafia LE
  Enzymology
    Roche Bioscience
    3401 Hillview Ave, S3-1, Palo Alto, CA 94304-1397, USA
    Tel: 650 354 7997
    Fax: 650 354 7554
    Email: liliana.scarafia@roche.com
  Full length single stranded sequencing of baited insert
  Insert Length: 2000 Std Error: 0.00
  Seq primer: primer 2 (5395)TACCACATCAATGATG; and insert-specific
  POLYA=yes.

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FEATURES
  source
  Location/Qualifiers
    1..1962
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="K142"
    /cell_type="keratinocyte"
    /cell_line="HaCat cell line; derived from long term primary
    human adult skin keratinocyte"
    /lab_host="yeast/E.coli"
    /clone_lib="human keratinocyte matchmaker cDNA library"
    /note="Vector: pACT2; Site 1: EcoRI; Site 2: XhoI;
    Matchmaker yeast two-hybrid system from Clontech; pACT2
    vector has GAL4 AD and HA epitope under ADH1 promoter.
    This oligo-dT primed library was screened with human
    Ubch5a as bait, to obtained interacting proteins."
  ORIGIN
    Query Match 91.1%; Score 1816.8; DB 6; Length 1962;
    Best Local Similarity 99.6%; Pred. No. 0;
    Matches 1853; Conservative 0; Mismatches 2; Indels 5; Gaps 3;
    QY 131 CAGCCCTTGCCCTCTTGATGATAGGACCTCTTGGAGAGCCAACTGTGTGAGATGG 190
    Db 108 CAGCCCTTGCCCTCTTGATGATAGGACCTCTTGGAGAGCCAACTGTGTGAGATGG 167
    QY 191 CAGCCCAAGTGTGCCCCGAGCAGATCAGGACCTTCTGGGCGAAGAGTCTCTCTGGGG 250
    Db 168 CAGCCCAAGTGTGCCCCGAGCAGATCAGGACCTTCTGGGCGAAGAGTCTCTCTGGGG 227
    QY 251 AAGCCAGCCATGCTGACCTGCTTCAAGACAGGCGCTCTGAGACCTCCTCAGCGCTGC 310
    Db 228 AAGCCAGCCATGCTGACCTGCTTCAAGACAGGCGCTCTGAGACCTCCTCAGCGCTGC 287
    QY 311 CTGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGCGAGAGCAACACAGATCTCGGGAG 370
    Db 288 CTGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGCGAGAGCAACACAGATCTCGGGAG 347
    QY 371 CGCTGCGAGAGCTTCTGCATTTTCAAGCCAGCCAGAGGGAGGAGAGAGTTCCTCATG 430
    Db 348 CGCTGCGAGAGCTTCTGCATTTTCAAGCCAGCCAGAGGGAGGAGAGAGTTCCTCATG 407
    QY 431 TGCAAGTTTCAGGAGGCGCAGGAACTGTTGAGAGACTCGGCCCTGGAGAGCTCGATCTG 490
    Db 408 TGCAAGTTTCAGGAGGCGCAGGAACTGTTGAGAGACTCGGCCCTGGAGAGCTCGATCTG 467
    QY 491 AAGAGCAGAGAGCAGGCTCTGCGGAGAGTGGAGCACTTGAAGAGATGCCAGCAGCAG 550
    Db 468 AAGAGCAGAGAGCAGGCTCTGCGGAGAGTGGAGCACTTGAAGAGATGCCAGCAGCAG 524
    QY 551 ATGGCTGAGGACAGGCTCTGTGAAGCCAGTGTGAGCTCTTCTCGGGAGCTGCGAG 610
    Db 525 ATGGCTGAGGACAGGCTCTGTGAAGCCAGGCTGTGAGAGTGTGAGAGCTGCGAG 584
    QY 611 GAGAGCCAGAGTCTGTTGAGAGGCTGCCACTAAGGAATGCCAGGCTCTGAGGCTCGGCC 670
    Db 585 GAGAGCCAGAGTCTGTTGAGAGGCTGCCACTAAGGAATGCCAGGCTCTGAGAGGCTCGGCC 644
    QY 671 CGGGCGGCGCAGCAGGAGCGCGGCTGTGAGAGTGTGAGAGGCTGTGAGAGGCTGTGAGCAGCAG 730
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    QY 731 CACAGCTGCTGAGTGTGAGCTGCGATCGAGGCGCAGAGCTGTGAGGCTCGGCTCGGC 790
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    QY 791 ATGAGCGCGCAGGCGCGCTCGGAGAGAGAGAGAAAGCTGGCCCAAGTGTGAGGCTCGGCTAT 850
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    QY 851 CACAGCTCTTCAAGAAATACGACACCAATCAAGAGAGCGGTGTGAGGAGTGTGAGGAG 910
    Db 825 CACAGCTCTTCAAGAAATACGACACCAATCAAGAGAGCGGTGTGAGGAGTGTGAGGAG 884

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QY 551 ATGCTGAGGACAAAGCCTCTGTGAAGCCACAGGTGACGTCTCTTCTCTGGGAGCTGCAG 610
DB 539 ATGCTGAGGACAAAGCCTCTGTGAAGCCACAGGTGACGTCTCTTCTCTGGGAGCTGCAG 598
QY 611 GAGAGCCAGAGTGCCTTGGAGGCTGCCACTAAGGAATGCGAGGCTCTGGAGGGTGGGCC 670
DB 599 GAGAGCCAGAGTGCCTTGGAGGCTGCCACTAAGGAATGCGAGGCTCTGGAGGGTGGGCC 658
QY 671 CGGGCGGCGAGCAGAGCGCGCGAGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 730
DB 659 CGGGCGGCGAGCAGAGCGCGCGAGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 718
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DB 839 CACAGCTCTTCCAAGAAATACGACACACATCAAGAGAGCGTGGTGGCGAGTGAAGCGG 898
QY 911 AAGC----GAGGAATGAGCTGGAAGATCTCAACAGAGCTCCAGAGCGCGGAGGAGGC 966
DB 899 AAGCGAGTGAAGATGAGCTGGAAGATCTCAACAGAGCTCCAGAGCGCGGAGGAGGC 958
QY 967 CTTGTGGGCAACAGAGAGTGAATGAAGCTGAAGAGGAGGCGGAGCAGCAAGAT 1026
DB 959 CTTGTGGGCAACAGAGAGTGAATGAAGCTGAAGAGGAGGCGGAGCAGCAAGAT 1018
QY 1027 TGTGATGAGAGCGCTTCCGCTGCTGAAGCCAGCGGATATCTACAGGCGGACTTCCA 1086
DB 1019 TGTGATGAGAGCGCTTCCGCTGCTGAAGCCAGCGGATATCTACAGGCGGACTTCCA 1078
QY 1087 GGCTGAGAGCGAGCGCGGAGAGCTGGCGAGAGAGAGAGTCTCTGAGGAGCAGCT 1146
DB 1079 GGCTGAGAGCGAGCGCGGAGAGCTGGCGAGAGAGAGAGTCTCTGAGGAGCAGCT 1138
QY 1147 GAGAGAGCTGAGAGGAGTACAGCAACTGAAGCCAGCTGTGAGGAGTGGCGAGGAT 1206
DB 1139 GAGAGAGCTGAGAGGAGTACAGCAACTGAAGCCAGCTGTGAGGAGTGGCGAGGAT 1198
QY 1207 CGAGGACATGAGGAAGCGGATGTGAGGTCTCCAGAGCCCTTGTCCCGCCCGCCCTGC 1266
DB 1199 CGAGGACATGAGGAAGCGGATGTGAGGTCTCCAGAGCCCTTGTCCCGCCCGCCCTGC 1258
QY 1267 CTACCTCTCTCTCCCTGGCCCTGCCAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1326
DB 1259 CTACCTCTCTCTCCCTGGCCCTGCCAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1318
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DB 1319 TGACTTCTGCTGTCAGAGTGCAGTATCAGGCGCTGATATGACACCTGCGAGATACA 1378
QY 1387 TGTATGAGTGCATGAGTAGGCGCGGCGAGTCAAGGCGCACTGCCTGCGCCGAGGAGCT 1446
DB 1379 TGTATGAGTGCATGAGTAGGCGCGGCGAGTCAAGGCGCACTGCCTGCGCCGAGGAGCT 1437
QY 1447 GCGCGGAGCGGTGAGTGTGCGCTTCTCTCCCGCTGCTAGCCAGGAGTGAAGGCT 1506
DB 1438 GCGCGGAGCGGTGAGTGTGCGCTTCTCTCCCGCTGCTAGCCAGGAGTGAAGGCT 1497
QY 1507 GGTGGCCACAACTGGGATGCCACCTGGAGCGCCACCCAGAGCTGGCGGCGGACCTTA 1566
DB 1498 GGTGGCCACAACTGGGATGCCACCTGGAGCGCCACCCAGAGCTGGCGGCGGACCTTA 1557
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DB 1558 CGCTTACGCTGTGATTCGCTGGTCCCTCTTTTGGGTAGATGCGGCGCCGATCAGGCC 1617
QY 1627 TGACTCGCTGCTCTTTTGTTCCTCTCTGTCTCGAACCACTTGCTCGGCTGGGCTAATCC 1686
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DB 1618 TGACTCGCTGCTCTTTTGTTCCTCTCTGTCTCGAACCACTTGCTCGGCTAATCC 1677
QY 1687 CTCCTCTTCTCCACCGGCACTGGGGAAGTCAAGAAATGGGCTCTGAGGGA 1746
DB 1678 CTCCTCTTCTCCACCGGCACTGGGGAAGTCAAGAAATGGGCTCTGAGGGA 1737
QY 1747 GAACTGCTTCCCTCGGAGAGCTGGGTGGAGCTTCTCCACCGGACACCGACCCGC 1806
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QY 1807 CCGCGCTGCTGGGAGAGTGGCTCTTACCATGCACACGGTGTCTCTCTTTGG 1866
DB 1798 CCGCTGCTGCTGGGAGTGGCTCTTACCATGCACACGGTGTCTCTCTTTGG 1857
QY 1867 GCTCATGCTATTCATTTTCAGCCAGACCGAGTGTATTTAACAGTCACTATTGATG 1926
DB 1858 GCTCATGCTATTCATTTTCAGCCAGACCGAGTGTATTTAACAGTCACTATTGATG 1917
QY 1927 GACATTTGGGTGTTTCCATCTTTT 1952
DB 1918 GACATTTGGGTGTTTCCCATCTTTT 1943

RESULT 5
CR603029 1751 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DC017YA10 of Neuroblastoma Cot
DEFINITION 25-normalized of Homo sapiens (human).
ACCESSION CR603029
VERSION CR603029.1 GI:50483836
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1751)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
REFERENCE 2 (bases 1 to 1751)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequenage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life technologies, a
division of Invitrogen.
FEATURES
source
1..1751
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC017YA10"
/tissue_type="Neuroblastoma Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 73.5%; Score 1466.4; DB 3; Length 1751;
Best Local Similarity 91.4%; Pred. No. 1.9e-302;
Matches 1641; Conservative 0; Mismatches 1; Indels 154; Gaps 2;

QY 131 CAGCCCTTGGCTGTTGGATGAATAGGCACCTCTGGAAGACCACTGTGTGAGATGGT 190
DB 110 CAGCCCTTGGCTGTTGGATGAATAGGCACCTCTGGAAGACCACTGTGTGAGATGGT 169
QY 191 CAGCCAGTGGTGGCGCGGAGCAGAGTCAAGAGTCTGCGGAGAGAGTCTCTCTGGG 250
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170	Db	 CAGCCCACTGCTGGCCCGCAGCAGATCAGACGCTACTGGCGCGAAGAGTCTCTCTCTGCGG	229
251	Qy	 AAGCCAGCATTGCTGCACCTGCCCTTCAGAA CAGGCGCTCTCTGAGACCTCTCAGCGCTGC	310
230	Db	 AAGCCAGCATTGCTGCACCTGCCCTTCAGAA CAGGCGCTCTCTGAGACCTCTCAGCGCTGC	289
311	Qy	 CTGAGGAGAAATCAAGAGCTCCGATGCCATCCGGCAGAGCAACCAAGATTCTCGGGAG	370
290	Db	 CTGGAGGAGAAATCAAGAGCTCCGATGCCATCCGGCAGAGCAACCAAGATTCTCGGGAG	349
371	Qy	 CGCTCGAGGAGCTTCTGCATTTCCAGCCAGACCCAGAGGAGGAGAGGAGTTCCTCATG	430
350	Db	 CGCTCGAGGAGCTTCTGCATTTCCAGCCAGACCCAGAGGAGGAGAGGAGTTCCTCATG	409
431	Qy	 TGCAGATTTCAGAGGAGCCAGGAAATCTGGTGGAGAGACTCGGCCCTGGAGAGCTCGATCTG	490
410	Db	 TGCAGATTTCAGAGGAGCCAGGAAATCTGGTGGAGAGACTCGGCCCTGGAGAGCTCGATCTG	469
491	Qy	 AAGAGGCAGAAAGGAGCAGGCTCTCGGGAGGTGGAGCACTTGAAGAGATGCCAGCAGCAG	550
470	Db	 AAGAGGCAGAAAGGAGCAGGCTCTCGGGAGGTGGAGCACTTGAAGAGATGCCAGCAGCAG	529
551	Qy	 ATGCTGAGGACAAGGCTCTGTGAAGCCACAGGTGAGCTCTTTGCTCGGGGAGCTGGAG	610
530	Db	 ATGCTGAGGACAAGGCTCTGTGAAGCCACAGGTGAGCTCTTTGCTCGGGGAGCTGGAG	589
611	Qy	 GAGAGCCAGAGTCTGCTTGGAGCTGCCACTAAGGAATGCCAGGCTCTGGAGGCTCGGGCC	670
590	Db	 GAGAGCCAGAGTCTGCTTGGAGCTGCCACTAAGGAATGCCAGGCTCTGGAGGCTCGGGCC	645
671	Qy	 CGGCGGCCCAGCAGCAGCGCGCGCAGCTGTGAGAGTGAAGCGCAGGCGCTGACAGCAGCAG	730
646	Db	----- -----	645
731	Qy	 CACAGCTGCAGGTGGACCACTCGGCCATGACAGGCCCAGAGCTGTGAGGCGCGCCTCGC	790
646	Db	----- -----	645
791	Qy	 ATGAGCGCCAGGCGCGCTCGGAGGAGAGGAAGCTGGCCCAAGTTGCAAGTTCAGGTCGCCCTAT	850
646	Db	----- -----GAGGAAGCTGGCCCCAGTTGCAAGTTCGCCCTAT	676
851	Qy	 CACAGCTCTTCCAAGAATACGACCAACATCAAGAGCAGCGTGTGGGCAGTGAGCGG	910
677	Db	 CACAGCTCTTCCAAGAATACGACCAACATCAAGAGCAGCGTGTGGGCAGTGAGCGG	736
911	Qy	 AAGCGAGAAATGACGTGTGAAGATCTCAAA CAGCAGCTCCAGCAGGCCGAGGAGGCCCTG	970
737	Db	 AAGCGAGAAATGACGTGTGAAGATCTCAAA CAGCAGCTCCAGCAGGCCGAGGAGGCCCTG	796
971	Qy	 GTGCCCCAACAGGAGGTGATCGATAAGCTGAAGGAGGCGCCGAGCAGCAACAGATTGTG	1030
797	Db	 GTGCCCCAACAGGAGGTGATCGATAAGCTGAAGGAGGCGCCGAGCAGCAACAGATTGTG	856
1031	Qy	 ATGAGACCCGTTCCGCTGCTGAAGCCCCCAGCGGATATCTACAAGCGGACTTCCAGGCT	1090
857	Db	 ATGAGACCCGTTCCGCTGCTGAAGCCCCCAGCGGATATCTACAAGCGGACTTCCAGGCT	916
1091	Qy	 GAGAGCAGGCCCCGGGAGAACTGGCCGAGAAAGAGGTCTCTGCAAGGAGCAGCTGGAG	1150
917	Db	 GAGAGCAGGCCCCGGGAGAACTGGCCGAGAAAGAGGTCTCTGCAAGGAGCAGCTGGAG	976
1151	Qy	 CAGCTGCAGAGGAGTACAGCAACTGAAGCCAGCTGTCAAGAGTTCGGCCAGGATCCAG	1210
977	Db	 CAGCTGCAGAGGAGTACAGCAACTGAAGCCAGCTGTCAAGAGTTCGGCCAGGATCCAG	1036
1211	Qy	 GACATGAGGAAGCGGCATGTGAGGTTCTCCAGGCCCTCTCCAGGCCCTTGGCCCCCGCCCTG	1270
1037	Db	 GACATGAGGAAGCGGCATGTGAGGTTCTCCAGGCCCTCTCCAGGCCCTTGGCCCCCGCCCTG	1096
1271	Qy	 CTCTCTCTCTCCCTGGCCCTGCCCAGCCAGAGGAGGAGCCCCCCCCCGAGGAGCCACTTGAC	1330

Db	1097	CTCTCTCTCTCCCTCGCCCTCTGCCAGCAGGAGGAGGAGCCCGGAGGAGCCACCTGAC	1151
Qy	1331	TTCTGCTGTCCCAAGTCGACAGTATCAGGCGCCCTGTATATGACACCCCTGACAGATACATGTC	1390
Db	1157	TTCTGCTGTCCCAAGTCGACAGTATCAGGCGCCCTGTATATGACACCCCTGACAGATACATGTC	1216
Qy	1391	ATGAGTGCATTTGATGAGGCGCGCCAGTCGAAAGGCCACTGCTTGCCTGCCGAGGACGTGCCCC	1450
Db	1217	ATGAGTGCATTTGATGAGGCGCGCCAGTCGAAAGGCCACTGCTTGCCTGCCGAGGACGTGCCCC	1275
Qy	1451	GGGACCGTCAGTGTGCGCTTCTCTCCCGCTGCTAGCCAGGATGAGGAGGCTGGGT	1510
Db	1276	GGGACCGTCAGTGTGCGCTTCTCTCCCGCTGCTAGCCAGGATGAGGAGGCTGGGT	1335
Qy	1511	GGCCACAACCTGGGATGACCTGAGAGCCACACAGGAGCTGCGCGGGCACCTTACGCT	1570
Db	1336	GGCCACAACCTGGGATGACCTGAGAGCCACACAGGAGCTGCGCGGGCACCTTACGCT	1395
Qy	1571	TCAGCTGTTGATCCGCTGGTCCCTCTCTTTTGGGGTAGATGCGGCCCGATCAGGCGCTGAC	1630
Db	1396	TCAGCTGTTGATCCGCTGGTCCCTCTCTTTTGGGGTAGATGCGGCCCGATCAGGCGCTGAC	1455
Qy	1631	TGCGTGTCTTTTGTTCCTTCTGTCTGTCTGTCGAAACCACTTGTGCTGGGGCTTAATCCCTCC	1690
Db	1456	TGCGTGTCTTTTGTTCCTTCTGTCTGTCTGTCGAAACCACTTGTGCTGGGGCTTAATCCCTCC	1515
Qy	1691	CTCTTCTCCACCGGCACCTGGGGAGTCAAGAAATGGGGCTCGGGGCTCTCAGGAGAAC	1750
Db	1516	CTCTTCTCCACCGGCACCTGGGGAGTCAAGAAATGGGGCTCTCAGGAGAAC	1575
Qy	1751	TGCTTCCCTCTGGCAGAGCTGGGTGGCAGCTCTTCTCTCCACCGGACACCGCCGCCGCGC	1810
Db	1576	TGCTTCCCTCTGGCAGAGCTGGGTGGCAGCTCTTCTCTCCACCGGACACCGCCGCCGCGC	1635
Qy	1811	CGCTGTGCCCTGGGAGTGTGCCCTCTTACCATGACACCGGGTCTCTCTTTTGGGCTG	1870
Db	1636	TGCTGTGCCCTGGGAGTGTGCCCTCTTACCATGACACCGGGTCTCTCTTTTGGGCTG	1695
Qy	1871	CATGCTATTCCATTTTTCAGCCAGACGATGTGTATTTAACCAAGTCACTATTTCATG	1926
Db	1696	CATGCTATTCCATTTTTCAGCCAGACGATGTGTATTTAACCAAGTCACTATTTCATG	1751
RESULT 6			
LOCUS	CR612085	1164 bp mRNA linear HTC 21-JUL-2004	
DEFINITION	Full-length cDNA clone CS0DJ015Vf17 of T cells (Jurkat cell line)		
	Cot 10-normalized of Homo sapiens (human).		
ACCESSION	CR612085		
VERSION	CR612085.1 GI:50492892		
KEYWORDS	HTC; CNSLT_CDNA.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1164)		
TITLE	Li W.B., Gruber, C., Jesse, J. and Polayes, D.		
JOURNAL	Full-length cDNA libraries and normalization		
REMARK	Unpublished		
	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600		
	Paraday Avenue		
REFERENCE	2 (bases 1 to 1164)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequençage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
	- Web : www.genoscope.cns.fr)		
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.		







[illegible]



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/clone lib="Homo sapiens PLACENTA"
/notes="Vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
ORIGIN

Query Match          46.0%; Score 916.8; DB 1; Length 1081;
Best Local Similarity 94.4%; Pred. No. 4.7e-185;
Matches 966; Conservative 20; Mismatches 33; Indels 4; Gaps 4;

QY 929 GAAGATCTCAACAGCAGCTCCAGCAGCGCCGAGGAGCCCTGTCGCCCAACAGCAGGTTG 988
DB 1020 GAAGTCTCAACAGCAGCTCCAGCAGCGCCGAGGAGCCCTGTCGCCCAACAGCAGGTTG 962
QY 989 ATCGATAAGCTGAAGGAGGAGCGCAGCAGCAC-AAGATTGTGATGGAGACCGTTCCCGT 1047
DB 961 ATCGATAAGCTGAAGGAGGAGCGCAGCAGCACAAAGATTGTGATGGAAGCGTTCCCGT 902
QY 1048 GCTGAAGGCCCGCGGATATCTACAGGCGGACTTCAGGCTGAGAGCAGGCCCGGGA 1107
DB 901 GCTGAAGGCCCGCGGATATCTACAGGCGGACTTCAGGCTGAGAGCAGGCCCGGGA 842
QY 1108 GAAGCTGGCCGAGAGAGGAGCTCTGAGGAGCAGCTGGAGCAGCTGCAGAGGAGTA 1167
DB 841 GAAGCTGGCCGAGAGAGGAGCTCTGAGGAGCAGCTGGAGCAGCTGCAGAGGAGTA 782
QY 1168 CAGCAACTGAAGCCAGCTGTGAGGAGTGGCCAGGATCGAGGACATGAGGAACGCGCA 1227
DB 781 CAGCAACTGAAGCCAGCTGTGAGGAGTGGCCAGGATCGAGGACATGAGGAACGCGCA 722
QY 1228 TGTGAGGCTCTCCAGGCGCCCTTGTGCGCCCGCCCTGCTACCTCTCTCTCCCTGCG 1287
DB 721 TGTGAGGCTCTCCAGGCGCCCTTGTGCGCCCGCCCTGCTACCTCTCTCTCCCTGCG 662
QY 1288 CTTGCCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1347
DB 661 CTTGCCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 602
QY 1348 CAGTATCAGGCGCCCTGATATGACACCTGTCAGATACATGTCATGAGTGATGAGTA 1407
DB 601 CAGTATCAGGCGCCCTGATATGACACCTGTCAGATACATGTCATGAGTGATGAGTA 542
QY 1408 GGGCGGCGCAGTGCAGAGGCACTGCTGCGCCAGAGCAGTCCCGGAGCCGTCGAGTCTGC 1467
DB 541 GGGCGGCGCAGTGCAGAGGCACTGCTGCGCCAGAGCAGTCCCGGAGCCGTCGAGTCTGC 483
QY 1468 GCTTCTCTCCGCTGCTAGCCAGAGTGAAGGCTGGGTGGCCCAACACTGGGATGC 1527
DB 482 GCTTCTCTCCGCTGCTAGCCAGAGTGAAGGCTGGGTGGCCCAACACTGGGATGC 423
QY 1528 CACCTGGAGCCACCCAGGAGCTGGCCGCGCAGCTTACGCTTCAGCTTGTGATCGCT 1587
DB 422 CACCTGGAGCCACCCAGGAGCTGGCCGCGCAGCTTACGCTTCAGCTTGTGATCGCT 363
QY 1588 GGTCCCTCTTTTGGGTAGATCGGCGCCCGGATCAGGCTGACTCGCTGCTCTTTTGT 1647
DB 362 GGTCCCTCTTTTGGGTAGATCGGCGCCCGGATCAGGCTGACTCGCTGCTCTTTTGT 303
QY 1648 CCGTCTGTCTGTGAACCACTTGGCTGGGCTTAATCCCTCTCTTCCACCCCGG 1707
DB 302 CCGTCTGTCTGTGAACCACTTGGCTGGGCTTAATCCCTCTCTTCCACCCCGG 243
QY 1708 ACTGGGGAAGTCAAGATGGGCGCTCTCAGGAGAGTCTTCCCTCCGCGAG 1767
DB 242 ACTGGGGAAGTCAAGATGGGCGCTCTCAGGAGAGTCTTCCCTCCGCGAG 183
QY 1768 CTGGGTGGCAGCTCTTCTTCCACCGGACACCGGACCCCGCGCGCTGTGCTTGGGAGT 1827
DB 182 CTGGGTGGCAGCTCTTCTTCCACCGGACACCGGACCCCGCGCGCTGTGCTTGGGAGT 123
QY 1828 GCTGCCCTCTTACCATGACACGGGTGCTCTCTTTTGGGCTGATGCTATTCCATTG 1887

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DB 122 GCTGCAACWACCAAGCACAC-GGAAAMAMAAWTCGGCAACATGMAATWCAATTTN 64
QY 1888 CAGCAGACCGATGTATTAAACAGTCACTATTGATGACATTTGGGTGTTTCCCAT 1947
DB 63 CABCAKACCGATGTTATTATTCYAGTATATTGATGATATTGTTGGTATCCCTTT 4
QY 1948 CTT 1950
DB 3 TTT 1

RESULT 11
BX325315/c
LOCUS
DEFINITION
  BX325315 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
  Homo sapiens cDNA clone CS0DL002YJ17 3-PRIME, mRNA sequence.
ACCESSION
  BX325315
VERSION
  BX325315.2 GI:46262968
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 1036)
  Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  Full-length cDNA libraries and normalization
  Unpublished (2001)
  On May 1, 2003 this sequence version replaced gi:30307434.
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
  Email: segret@genoscope.cns.fr, Web : www.genoscope.cns.fr
  1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
  end enriched, double-strand cDNA was digested with Not I and cloned
  into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
  was normalized. Library was constructed by Life Technologies, a
  division of Invitrogen. This sequence belongs to sequence cluster
  10873.f
  For more information about this cluster, see
  http://www.genoscope.cns.fr/cdna?s=CS0AL002CE09NP1&c=10873.f.
  Location/Qualifiers
    1..1036
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="CS0DL002YJ17"
      /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
      /cell_line="RAMOS CELL LINE"
      /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
      25-NORMALIZED"
      /note="1st strand cDNA was primed with a NotI-oligo(dT)
      primer. Five prime end enriched, double-strand cDNA was
      digested with Not I and cloned into the Not I and EcoRV
      sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match          45.8%; Score 914.2; DB 5; Length 1036;
Best Local Similarity 96.8%; Pred. No. 1.7e-184;
Matches 969; Conservative 5; Mismatches 23; Indels 4; Gaps 4;

QY 967 CCTGGTGGCCAAACAGGAGGTGATCGATAAGCTGAAGGAGGAGCCGAGCAGCAAGAT 1026
DB 998 CCTGTGKCCACAGCAGA-GTGTGATAGTATGCTAGAGGAGA-GCCGAGCAGCAGAT 941
QY 1027 TGTGATGAGACCGTTCCTCCGTGCTGAAGCCCGGATATCTTACAGGCGGACTTCCA 1086
DB 940 TGTGATGAGAC-CGGTTCCTGCTGAAGCCCGGATATCTTACAGGCGGACTTCCA 882
QY 1087 GGTGATGAGACCGCCGCGGAGAGCTGCGGAGAGAGAGGCTCTGAGGAGCAGCT 1146
DB 881 GGTGATGAGACCGCCGCGGAGAGAGCTGCGGAGAGAGAGGCTCTGAGGAGCAGCT 822

```



Db 678 GCACAGCGTCAGGGTGGACCACTGGGCATGACGGCCAGAGCGTGGAGGCGCGCTCC 737  
 Qy 789 GCATGGAGCCGAGCGCGCTCGGAGGAGAGGAGTGGCCAGTTGCAAGTGGCT 848  
 Db 738 GCATGGAGCCGAGCGCGCTCGGAGGAGAGGAGTGGCCAGTTGCAAGTGGCT 797  
 Qy 849 ATACCAAGCTCTTCCAGAGATACGACCAACACATCAAGAGCAGCGTGGTGGCAGTGAGC 908  
 Db 798 ATACCAAGCTCTTCCAGAGATACGACCAACACATCAAGAGCAGCGTGGTGGCAGTGAGC 857  
 Qy 909 GGAAGCGAGGAATGCAGCTGGAGATCTCAAAACAGCAGCTCCAGAGCGCCGAGGAGGCC 968  
 Db 858 GGAACAGGTGAATGCAGCTGGAGATCTC-AACAGCAGCTCCAGAGCGCCGAGGAGGCC 916  
 Qy 969 TGGTGGCCAAACAGGAGGTATCGATAAGCTGAAGAGGAGCGGAGCAGCAGCAAGATTG 1028  
 Db 917 TGGTGGCCAAACAGGAGGTATCGATAAGCTGAAGAGGAGCGGAGCAGCAGCAAGATTG 976  
 Qy 1029 TGATGGAGACCGTTCCGGTGTGTAAGCGCCAGCGGATATCTCAAGCGGACTTCCAGG 1088  
 Db 977 TTAATGGAGACGTCCGGTGTGTAAGCGCCAGCGGATATCTGMAAGGGGACTT-CAGG 1035  
 Qy 1089 CTGAGAGGAGCGCCGAGGAGTGGCCGAGAGAGGAGTCTCTGAGGAGCAGCTGG 1148  
 Db 1036 CTGAGAGGAGCGCCGAGGAGTGGCCGAGAGAGGAGTCTCTGMAAGGGGACTT-CAGG 1092  
 Qy 1149 AGCAG 1153  
 Db 1093 YGCRG 1097

## RESULT 13

## BO674261

LOCUS DEFINITION BO674261 908 bp mRNA linear EST 15-JUL-2002  
 AGENCOURT\_8349206 NIH\_MGC\_102 Homo sapiens cDNA clone IMAGE:6276126  
 5', mRNA sequence.

## ACCESSION

BO674261

## VERSION

BO674261.1 GI:21785095

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 908)

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLC2460 row: 9 column: 07

High quality sequence stop: 711.

Location/Qualifiers

1..908

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6276126"

/tissue\_type="epidermoid carcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_102"

/note="Organ: salivary gland; Vector: pOTB7; Site\_1: XhoI;

Site\_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Library constructed

by Ling Hong in the laboratory of Gerald M. Rubin

(University of California, Berkeley) using ZAP-CDNA

## FEATURES

source

synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 44.0%; Score 877.6; DB 5; Length 908;  
 Best Local Similarity 99.3%; Pred. No. 1.1e-176;  
 Matches 902; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Qy 834 AGTTGCAGTGGCTTATCACCAGCTCTTCCAAAGATACGACCAACACATCAAGAGCAGCG 893  
 Db 1 AGTTGCAGTGGCTTATCACCAGCTCTTCCAAAGATACGACCAACACATCAAGAGCAGCG 60  
 Qy 894 TGGTGGCAGTGGAGCGGAAATGCAAGTGAAGATCTTCAAAACAGCAGCTCCAGC 953  
 Db 61 TGGTGGCAGTGGAGCGGAAATGCAAGTGAAGATCTTCAAAACAGCAGCTCCAGC 120  
 Qy 954 AGGCCGAGGAGGCGCTGGTGGCCAAACAGGAGGTGATCGATAAGCTGAAGGAGGAGCGCG 1013  
 Db 121 AGGCCGAGGAGGCGCTGGTGGCCAAACAGGAGGTGATCGATAAGCTGAAGGAGGAGCGCG 180  
 Qy 1014 AGCAGCACAAAGATTGTGATGGAGACCGTTCCGGTGTGAAAGCGCCAGCGGATATCTACA 1073  
 Db 181 AGCAGCACAAAGATTGTGATGGAGACCGTTCCGGTGTGAAAGCGCCAGCGGATATCTACA 240  
 Qy 1074 AGCCGAGTTCAGGCTGAGAGGAGCGCCCGGAGAGAGTGGCCGAGAGAGGAGCTCC 1133  
 Db 241 AGCCGAGTTCAGGCTGAGAGGAGCGCCCGGAGAGAGTGGCCGAGAGAGGAGCTCC 300  
 Qy 1134 TGCAGGAGCAGCTGAGCAGCTGCAGAGGAGTACAGCAACTGAAGCCAGAGGAGGAGCTCAGG 1193  
 Db 301 TGCAGGAGCAGCTGAGCAGCTGCAGAGGAGTACAGCAACTGAAGCCAGAGGAGGAGCTCAGG 360  
 Qy 1194 AGTGGCCAGGATGAGGACATGAGGAGCGGACATGTCGAGGTCTCCAGAGCCCGCTTGC 1253  
 Db 361 AGTGGCCAGGATGAGGACATGAGGAGCGGACATGTCGAGGTCTCCAGAGCCCGCTTGC 420  
 Qy 1254 CCCCAGCCCGCTGCTACCTCTCTCTCCCTGGCCCTGCCAGCAGGAGGAGGAGCCCGC 1313  
 Db 421 CCCCAGCCCGCTGCTACCTCTCTCTCCCTGGCCCTGCCAGCAGGAGGAGGAGCCCGC 480  
 Qy 1314 CCGAGGAGCCACCTGACTTCTGTGTCTCCAAAGTGCAGATATCAGGCGCCCTCATATGGACA 1373  
 Db 481 CCGAGGAGCCACCTGACTTCTGTGTCTCCAAAGTGCAGATATCAGGCGCCCTCATATGGACA 540  
 Qy 1374 CCCTGCAGATACATGTCATGAGTGCATGAGTGGCCGAGCCAGTGCAGGAGGAGGAGCTGCC 1433  
 Db 541 CCCTGCAGATACATGTCATGAGTGCATGAGTGGCCGAGCCAGTGCAGGAGGAGGAGCTGCC 600  
 Qy 1434 TGCCCGAGGAGCTGCCCGGAGCCGTGCAGTCTGCGCTTCTCTCCCGCTGCTAGGCC 1493  
 Db 601 TG-CCGAGGAGCTGCCCGGAGCCGTGCAGTCTGCGCTTCTCTCCCGCTGCTAGGCC 659  
 Qy 1494 AGGATGAAGGGCTGGGTGGCCCAACTGGGATGCACCTGGAGCCCGCCAGGAGGAGTGG 1553  
 Db 660 AGGATGAAGGGCTGGGTGGCCCAACTGGGATGCACCTGGAGCCCGCCAGGAGGAGTGG 719  
 Qy 1554 CCGGGGACCTTACGCTTACGCTTGTGATCCGCTGCTCCCTCTTTTGGGGGTAGATGGG 1613  
 Db 720 CCGGGGACCTTACGCTTACGCTTGTGATCCGCTGCTCTCTTTTGGGGGTAGATGGG 779  
 Qy 1614 CCCCAGTACAGGCGCTGACTCGCTCTCTTTTGTGTCTCTCTCTCTGCTGCTGCAACCACTTGC 1673  
 Db 780 CCCCAGTACAGGCGCTGACTCGCTCTCTTTTGTGTCTCTCTCTCTGCTGCTGCAACCACTTGC 838  
 Qy 1674 CTGGGGTATCTCCCT 1733  
 Db 839 CTGGGGTATCTCCCT 898  
 Qy 1734 GGGCTCTC 1741  
 Db 899 GGGCTCTC 906







GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 8, 2005, 12:25:23 ; Search time 1097 Seconds  
(without alignments)  
10760.223 Million cell updates/sec

Title: US-09-377-795-1  
Perfect score: 1994  
Sequence: 1 ggcacgagcagcgcccttgt.....gtataaaaaaaaaaaaaa 1994

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003as:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004as:\*

13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1994	100.0	1994	3 AAC81426	Aac81426 Human I-k
2	1994	100.0	1994	3 AAA35027	Aaa35027 Human ade
3	1994	100.0	1994	3 AAF21149	Aaf21149 Human low
4	1994	100.0	1994	8 ADA44705	Ada44705 Human inh
5	1994	100.0	1994	10 ABZ96843	Abz96843 Human nuc
6	1994	100.0	1994	10 ABV75393	Abv75393 Human NEM
7	1994	100.0	1994	11 ABD20692	Abd20692 Human pul
8	1994	100.0	8631	3 AAA35028	Aaa35028 Human ade
9	1994	100.0	8631	3 AAF21150	Aaf21150 Human low
10	1994	100.0	8631	10 ABZ96844	Abz96844 Human nuc
11	1992.4	99.9	8631	11 ABD20693	Abd20693 Human pul
12	1954.4	98.0	1967	13 ADQ87415	Adq87415 Human tum
13	1954.4	98.0	1967	13 ADQ86256	Adq86256 Human tum
14	1836.4	92.1	2035	8 ADQ82012	Adq82012 Human NEM
15	1832.6	91.9	1975	8 ADA44712	Ada44712 Human inh
16	1823	91.4	2009	2 AAZ07513	Aaz07513 Human RFP
17	1757.2	88.1	2034	2 AAZ07514	Aaz07514 Human RFP
18	1358.6	68.1	2038	10 ADF82713	Adf82713 Leukaemia
19	1253.6	62.9	1260	12 ADK71964	Adk71964 Human I K
20	941	47.2	1104	13 ADS17862	Ads17862 Human IKB

21	940.4	47.2	1874	10 ADC36537	Adc36537 DNA encod
22	940.4	47.2	1874	12 ADI61940	Adi61940 Necrosis
23	940.4	47.2	1874	12 ADI29002	Adi29002 Human NEM
24	940.4	47.2	1874	13 ADI61943	Adi61943 Necrosis
25	705.8	35.4	23106	9 ACD23011	Acd23011 Human NEM
26	486	24.4	486	13 ADS17866	Ads17866 Human IKB
27	402.6	20.2	483	13 ADS17864	Ads17864 Human IKB
c	277.6	13.9	2803	3 AAF21697	Aaf21697 Human bre
29	262	13.1	337	10 ADF81343	Adf81343 Leukaemia
30	216	10.8	597	12 ACH79507	Ach79507 Human gen
31	212	10.6	236	9 ACH15127	Ach15127 Human adu
32	207.4	10.4	526	12 ACH76707	Ach76707 Human gen
33	207	10.4	211	12 ACH93207	Ach93207 Human gen
34	195.4	9.8	197	12 ACH90407	Ach90407 Human gen
35	187	9.4	264	13 ADS17868	Ads17868 Human IKB
c	155.6	7.8	30191	12 ADQ97654	Adq97654 Mouse can
37	137	6.9	1926	3 AAAS0254	Aaas0254 Epstein B
38	137	6.9	1926	4 AAF82902	Aaf82902 EBV tethe
39	137	6.9	1926	10 ADK65580	Adk65580 Human her
40	137	6.9	2580	3 AAA75454	Aaa75454 Nucleotid
41	137	6.9	2580	6 AAI64275	Aai64275 Epstein-B
c	137	6.9	5452	2 AAX90923	Aax90923 Anti-sens
c	137	6.9	8705	2 AAZ23778	Aaz23778 Vector ps
c	137	6.9	8705	12 ADM10659	Adm10659 Expressio
c	137	6.9	9482	12 ADP64415	Adp64415 Vector pc

ALIGNMENTS

RESULT 1  
AAC81426  
ID AAC81426 standard; cDNA; 1994 BP.

XX AAC81426;

XX 23-FEB-2001 (first entry)

XX Human I-kappa-B kinase gamma-subunit (IKK-gamma) cDNA.

XX Human; I-kappa-B kinase; IKK; antisense therapy; gene therapy;  
KW cytokine expression inhibition; NF-kappa-B activation inhibition;  
KW nuclear factor-kappa-B; rheumatoid arthritis; immune disorder; cancer;  
KW IKK-gamma; gamma-subunit; ss.

XX Homo sapiens.

XX JP2000253884-A.

XX 19-SEP-2000.

PF 10-MAR-1999; 99JP-00063291.

XX 10-MAR-1999; 99JP-00063291.

XX (TOAG ) TOA COSEI CHEM IND LTD.

XX WPI; 2000-658913/64.

XX Antisense nucleic acid compound complementary to the subunit of IkappaB, used to treat rheumatic arthritis, immune diseases and cancer.

XX Claim 3; Page 14-15; 20pp; Japanese.

XX The invention relates to an antisense oligonucleotide targetted to a gene encoding a subunit of I-kappa-B kinase (IKK) which inhibits its expression, and thereby inhibits expression of a cytokine such as IL-6 (interleukin-6). I-kappa-B kinase activates NF-kappa-B (nuclear factor-kappa-B) which acts as a transcriptional regulator of cytokine genes. The antisense oligonucleotide can be used in gene therapy to treat rheumatoid arthritis, immune disorders and cancers. Sequences AAC81422-C81426 are cDNAs derived from genes whose expression may be inhibited using an antisense oligonucleotide of the invention. The present sequence

CC represents a human IKK-gamma subunit cDNA  
XX Sequence 1994 BP; 429 A; 585 C; 633 G; 347 T; 0 U; 0 Other;  
SQ Query Match 100.0%; Score 1994; DB 3; Length 1994;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACGAGCATGCCCCCTTGTGATCCAGGTGGGAAACTTAAGCCCCCAGAGAAAGTAGGACC 60  
Db 1 GGCACGAGCATGCCCCCTTGTGATCCAGGTGGGAAACTTAAGCCCCCAGAGAAAGTAGGACC 60

QY 61 CCCAGACATATCAATCCCACTCTCTCCCTCACTCCCTGTAAGCTCTCCAGCATATC 120  
Db 61 CCCAGACATATCAATCCCACTCTCTCCCTCACTCCCTGTAAGCTCTCCAGCATATC 120

QY 121 GAGGTCCCATAGCCCTTCCCTGTTGGATGAATAGGCACCTCTGGAAGAGCCAACTGTG 180  
Db 121 GAGGTCCCATAGCCCTTCCCTGTTGGATGAATAGGCACCTCTGGAAGAGCCAACTGTG 180

QY 181 TGAGATGTTGACAGCCAGTGGTGGCCCGCAGCAGATCAGAGACGTACTGGGCGAAGATC 240  
Db 181 TGAGATGTTGACAGCCAGTGGTGGCCCGCAGCAGATCAGAGACGTACTGGGCGAAGATC 240

QY 241 TCCTCTGGGGAAAGCCAGCCATGCTGCACCTGCTTTAGAAACAGAGCGCTCTCTGAGACCT 300  
Db 241 TCCTCTGGGGAAAGCCAGCCATGCTGCACCTGCTTTAGAAACAGAGCGCTCTCTGAGACCT 300

QY 301 CMAGCCCTGCTGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACCCAGAT 360  
Db 301 CMAGCCCTGCTGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACCCAGAT 360

QY 361 TCTGCGGAGCCCTCGGAGGACTTCTGATTTCAAGCCAGCCAGGAGGAGAGGA 420  
Db 361 TCTGCGGAGCCCTCGGAGGACTTCTGATTTCAAGCCAGCCAGGAGGAGAGGA 420

QY 421 GTTCTCTCATGTGCAAGTTCCAGAGGCGCAGGAACTGGTGAGAGACTCGGCTTGGAGAA 480  
Db 421 GTTCTCTCATGTGCAAGTTCCAGAGGCGCAGGAACTGGTGAGAGACTCGGCTTGGAGAA 480

QY 481 GCTCGATCTGAAGAGCGCAGAGGAGCGCTTGGGAGGTGGAGCACTTGAAGAGATG 540  
Db 481 GCTCGATCTGAAGAGCGCAGAGGAGCGCTTGGGAGGTGGAGCACTTGAAGAGATG 540

QY 541 CCAGCAGCAGATGCTGAGGACCAAGGCTCTGTGAAGCCAGGTGAGCACTTGTCTCGG 600  
Db 541 CCAGCAGCAGATGCTGAGGACCAAGGCTCTGTGAAGCCAGGTGAGCACTTGTCTCGG 600

QY 601 GGAGCTGACGAGAGCCAGAGTCTGAGGCTGCCACTAAGGAATGCCAGGCTCTTGA 660  
Db 601 GGAGCTGACGAGAGCCAGAGTCTGAGGCTGCCACTAAGGAATGCCAGGCTCTTGA 660

QY 661 GGGTGGGCGCGCGCCAGGAGCAGCGCGCGGAGCTGAGAGTGAAGCGCGGCT 720  
Db 661 GGGTGGGCGCGCGCGCCAGGAGCAGCGCGCGGAGCTGAGAGTGAAGCGCGGCT 720

QY 721 GCAGCAGCAGCAGCAGCTGAGGTGAGCAGCTGGCATGCGAGCCAGAGCGTGGAGGC 780  
Db 721 GCAGCAGCAGCAGCAGCTGAGGTGAGCAGCTGGCATGCGAGCCAGAGCGTGGAGGC 780

QY 781 CGCGTCCGCATGAGGCCAGCGCGCTCGAGGAGAGAGGAGAGCTGGCCCACTTGA 840  
Db 781 CGCGTCCGCATGAGGCCAGCGCGCTCGAGGAGAGAGGAGAGCTGGCCCACTTGA 840

QY 841 GGTGCGCTATCAGCAGCTCTTCCAGATACGAAACCAATCAAGAGCAGCGTGGG 900  
Db 841 GGTGCGCTATCAGCAGCTCTTCCAGATACGAAACCAATCAAGAGCAGCGTGGG 900

QY 901 CAGTGAGCGGAGGAGGAGATGCAAGTCTCAAAACAGCAGCTCCAGCAGGCGCA 960  
Db 901 CAGTGAGCGGAGGAGGAGATGCAAGTCTCAAAACAGCAGCTCCAGCAGGCGCA 960

QY 961 GGAGGCCCTGTGGCCAAACAGGAGGTGATCGATAAGAGGAGGAGGCCAGCAGCA 1020

RESULT 2





Db 1 GGCACGAGCATGGCCCTTGTGATCCAGGTGGGAAAATAAGGCCCCAGAGAAAGTCAGGACC 60  
Qy 61 CCGCAGACTATCAATCCAGTCTCTCCCTCACTCCCTGTGAAGCTCTCCAGCATATC 120  
Db 61 CCGCAGACTATCAATCCAGTCTCTCCCTCACTCCCTGTGAAGCTCTCCAGCATATC 120  
Qy 121 GAGGTCCCATCAGCCCTTCCCTGTGATGAATAGGCACCTCTGGAAGAGCAACTGTG 180  
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Qy 181 TGAGATGTGACGCCAGTGTGGCCCGCAGCAGATCAGACGTAATCTGAGGCGAAGATGTC 240  
Db 181 TGAGATGTGACGCCAGTGTGGCCCGCAGCAGATCAGACGTAATCTGAGGCGAAGATGTC 240  
Qy 241 TCCCTCTGGGGAAGCAGCCATGCTGCACCTGCTTTCAGAAACAGGGCGCTCTGAGACCT 300  
Db 241 TCCCTCTGGGGAAGCAGCCATGCTGCACCTGCTTTCAGAAACAGGGCGCTCTGAGACCT 300  
Qy 301 CCAGCGCTGCTGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGCGCAGAGCAACAGAT 360  
Db 301 CCAGCGCTGCTGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGCGCAGAGCAACAGAT 360  
Qy 361 TCTGCGGAGCGCTGCGAGAGCTTCTGATTTTCAAGCCAGCAGAGGAGGAGAAAGGA 420  
Db 361 TCTGCGGAGCGCTGCGAGAGCTTCTGATTTTCAAGCCAGCAGAGGAGGAGAAAGGA 420  
Qy 421 GTTCTCATGTGCAAGTTCCAGAGGCCAGGAACTGGTGGAGAGACTCGGCTCGAGAA 480  
Db 421 GTTCTCATGTGCAAGTTCCAGAGGCCAGGAACTGGTGGAGAGACTCGGCTCGAGAA 480  
Qy 481 GCTCGATCTGAAGAGCGCAGAGAGCAGGCTCTGCGGAGGTGGAGACCTCAAGAGATG 540  
Db 481 GCTCGATCTGAAGAGCGCAGAGAGCAGGCTCTGCGGAGGTGGAGACCTCAAGAGATG 540  
Qy 541 CCAGCAGCAGATGCTGAGGAAAGAGCTCTGTGAAAGCCAGAGTGAAGTCTGCTCGG 600  
Db 541 CCAGCAGCAGATGCTGAGGAAAGAGCTCTGTGAAAGCCAGAGTGAAGTCTGCTCGG 600  
Qy 601 GGAGCTGCAAGGAGAGCAGAGTCTGAGAGCTGCCATAGGAATGCCAGGCTCTGGA 660  
Db 601 GGAGCTGCAAGGAGAGCAGAGTCTGAGAGCTGCCATAGGAATGCCAGGCTCTGGA 660  
Qy 661 GGGTGGGCGCCGGGCGGCGCAGCAGCGCGGCGAGCTGGAGAGTGAAGCGAGCGCT 720  
Db 661 GGGTGGGCGCCGGGCGGCGCAGCAGCGCGGCGAGCTGGAGAGTGAAGCGAGCGCT 720  
Qy 721 GCAGCAGCAGCAGCGTGCAGGTGAGCAAGCAGCTGCGCATGCAAGGCGCAGAGCGTGGAGGC 780  
Db 721 GCAGCAGCAGCAGCGTGCAGGTGAGCAAGCAGCTGCGCATGCAAGGCGCAGAGCGTGGAGGC 780  
Qy 781 CGGCTCCGCATGGAGCGCGCGCGCTCGGAGGAGAGAGAGCTGGCCCAAGTGA 840  
Db 781 CGGCTCCGCATGGAGCGCGCGCGCTCGGAGGAGAGAGAGCTGGCCCAAGTGA 840  
Qy 841 GGTGGCTATCACAGCTCTTCCAGAAATACAGCAACCAATCAAGAGCAGCGTGGTGGG 900  
Db 841 GGTGGCTATCACAGCTCTTCCAGAAATACAGCAACCAATCAAGAGCAGCGTGGTGGG 900  
Qy 901 CAGTGAGCGGAAGCGAGGAATCAGCTGGAAGATCTCAAAAGCAGCTCCAGCAGGCCGA 960  
Db 901 CAGTGAGCGGAAGCGAGGAATCAGCTGGAAGATCTCAAAAGCAGCTCCAGCAGGCCGA 960  
Qy 961 GGAGGCCCTGGTGGCCCAACAGAGGTGATCGATTAAGCTGGAAGGAGGAGGCCGAGCAGCA 1020  
Db 961 GGAGGCCCTGGTGGCCCAACAGAGGTGATCGATTAAGCTGGAAGGAGGAGGCCGAGCAGCA 1020  
Qy 1021 CAAGATTGTGAGGAGACCGTTCAGAGGCGCCAGGCGGATATCTACAAGCGGA 1080  
Db 1021 CAAGATTGTGAGGAGACCGTTCAGAGGCGCCAGGCGGATATCTACAAGCGGA 1080  
Qy 1081 CTTCCAGGCTGAGAGCAGCGCCCGGAGAGCTGGCCGAGAAAGAGAGCTCTCTCAGGA 1140  
Db 1081 CTTCCAGGCTGAGAGCAGCGCCCGGAGAGAGCTGGCCGAGAAAGAGAGCTCTCTCAGGA 1140

## RESULT 4

ADA44705

ID ADA44705 standard; DNA; 1994 BP.

XX ADA44705;

XX ADA44705;

DT 20-NOV-2003 (first entry)

XX Human inhibitor-kappa B kinase-gamma encoding DNA #SEQ ID 3.

DE Antisense oligonucleotide; cytostatic; immunosuppressive;

XX

KW



KW antiinflammatory; gene therapy; hyperproliferative disorder; cancer;  
 KW autoimmune; inflammatory disorder; inhibitor-kappa B kinase-gamma; gene;  
 ds.

XX Homo sapiens.

XX WO2003031576-A2.

XX 17-APR-2003.

XX 03-OCT-2002; 2002WO-US031809.

XX 06-OCT-2001; 2001US-00972607.

XX (ISIS-) ISIS PHARM INC.

XX Monia BP, Wyatt JP;

XX WPI; 2003-457242/43.

XX New compound having sequence targeted to nucleic acid encoding inhibitor-kappa B kinase-gamma, useful for preparing composition for treating e.g., cancer, or inflammatory or autoimmune disorder.

XX Example 15; Page 82-85; 106pp; English.

CC The invention relates to an antisense compound that is targeted to a nucleic acid encoding inhibitor-kappa B kinase-gamma, specifically hybridizing to the nucleic acid encoding inhibitor-kappa B kinase-gamma and inhibiting its expression. Compounds of the invention are antisense oligonucleotides comprising at least one modified internucleoside linkage, which is a phosphorothioate linkage, at least one modified sugar moiety, which is a 2'-O-methoxyethyl sugar moiety, or at least one modified nucleobase, which is a 5-methylcytosine. Preferably, the antisense oligonucleotide is a chimeric oligonucleotide. The compound of the invention is useful for preparing a composition for treating a hyperproliferative disorder e.g., cancer, or an autoimmune or inflammatory disorder. The methods are useful for inhibiting the expression of inhibitor-kappa B kinase-gamma in cells or tissues, and treating an animal having a disease or condition associated with inhibitor-kappa B kinase-gamma. The current sequence represents the human inhibitor-kappa B kinase-gamma encoding sequence that was used to design the antisense oligonucleotides of the invention.

XX Sequence 1994 BP; 429 A; 585 C; 633 G; 347 T; 0 U; 0 Other;

Query Match 100.0%; Score 1994; DB 8; Length 1994;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACGAGATGGCCCTTGTGATCCAGTGGGAACTAAGGCCAGAGAGTGAGGACC 60  
 DB 1 GGCACGAGATGGCCCTTGTGATCCAGTGGGAACTAAGGCCAGAGAGTGAGGACC 60

QY 61 CCGCAGATATCAATCCAGTCTCTCCCTCACTCCCTGTGAAGTCTCCAGCATATC 120  
 DB 61 CCGCAGATATCAATCCAGTCTCTCCCTCACTCCCTGTGAAGTCTCCAGCATATC 120

QY 121 GAGGTCCCATCAGCCCTTGGCCCTGTGGATGAATAGGACCTCTGGAGAGCCAACTGTG 180  
 DB 121 GAGGTCCCATCAGCCCTTGGCCCTGTGGATGAATAGGACCTCTGGAGAGCCAACTGTG 180

QY 181 TGAGTGTGTGAGCCAGTGTGGCCCGGAGCAGATCAGGAGTACTGGGCGAAGATC 240  
 DB 181 TGAGTGTGTGAGCCAGTGTGGCCCGGAGCAGATCAGGAGTACTGGGCGAAGATC 240

QY 241 TCCTCTGGGGAAGCAGCCATGTGTGACCTTCCAGACAGGCGCTCTGAGACCCCT 300  
 DB 241 TCCTCTGGGGAAGCAGCCATGTGTGACCTTCCAGACAGGCGCTCTGAGACCCCT 300

QY 301 CCAGCGTGTCTGAGGAGATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACCCAGAT 360  
 DB 301 CCAGCGTGTCTGAGGAGATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACCCAGAT 360

QY 361 TCTCGGAGCGCTGCGAGAGCTTCTGCAATTTCCAGCCAGCCAGAGGGAGGAAGA 420  
 DB 361 TCTCGGAGCGCTGCGAGAGCTTCTGCAATTTCCAGCCAGCCAGAGGGAGGAAGA 420

QY 421 GTTCTCATGTGCAAGTTCCAGAGGCCAGGAAACTGTGTGAGAGACTCGGCTTGAGAA 480  
 DB 421 GTTCTCATGTGCAAGTTCCAGAGGCCAGGAAACTGTGTGAGAGACTCGGCTTGAGAA 480

QY 481 GCTCGATCTGAAGAGCAGAGAGGAGGAGGCTCTCGGGGAGGTGAGACACCTGAAGATG 540  
 DB 481 GCTCGATCTGAAGAGCAGAGAGGAGGAGGCTCTCGGGGAGGTGAGACACCTGAAGATG 540

QY 541 CCAGCAGCATGTGCTCAGGACCAAGGCTCTGTGAAGCCAGGTGAGCTCTTCTCTCGG 600  
 DB 541 CCAGCAGCATGTGCTCAGGACCAAGGCTCTGTGAAGCCAGGTGAGCTCTTCTCTCGG 600

QY 601 GGAGCTGCAGGAGCCAGAGTCTGTTGGAGGCTGCCACTAAGGAATGCCAGGCTCTTGG 660  
 DB 601 GGAGCTGCAGGAGCCAGAGTCTGTTGGAGGCTGCCACTAAGGAATGCCAGGCTCTTGG 660

QY 661 GGGTTCGGGCCCCGGGCGGCGCAGCAGCAGGCGCGGCGAGCTCGAGAGTGCAGCGGAGG 720  
 DB 661 GGGTTCGGGCCCCGGGCGGCGCAGCAGCAGGCGCGGCGAGCTCGAGAGTGCAGCGGAGG 720

QY 721 GCAGCAGCAGCAGCAGCGTGCAGGTGACCAAGTTCGCGATCGAGGCCAGAGCGTGGAGGC 780  
 DB 721 GCAGCAGCAGCAGCAGCGTGCAGGTGACCAAGTTCGCGATCGAGGCCAGAGCGTGGAGGC 780

QY 781 CCGCTTCGGATCGAGCGGCGGCGCAGCAGCAGGCGCGGCGAGTGCAGCGGAGGAGGAGG 840  
 DB 781 CCGCTTCGGATCGAGCGGCGGCGCAGCAGCAGGCGCGGCGAGTGCAGCGGAGGAGGAGG 840

QY 841 GGTGGCTTATCAACAGCTCTTCCAGGAATACGACCAACCATCAAGAGCAGCGTGGTGGG 900  
 DB 841 GGTGGCTTATCAACAGCTCTTCCAGGAATACGACCAACCATCAAGAGCAGCGTGGTGGG 900

QY 901 CAGTGCAGCGGAGCGAGGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 960  
 DB 901 CAGTGCAGCGGAGCGAGGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 960

QY 961 GGAGGCCCTGTGTGGCCCAACAGGAGGTGATCGATAAGCTGAAGAGGAGGCCAGAGCAGCA 1020  
 DB 961 GGAGGCCCTGTGTGGCCCAACAGGAGGTGATCGATAAGCTGAAGAGGAGGCCAGAGCAGCA 1020

QY 1021 CAGATTGTGATGAGACCGTTCGGTGTCTGAAGCCCGAGGCGGATATCTACAAGGCGGA 1080  
 DB 1021 CAGATTGTGATGAGACCGTTCGGTGTCTGAAGCCCGAGGCGGATATCTACAAGGCGGA 1080

QY 1081 CTTTCCAGGCTGAGAGCGAGCGGCCGAGAGAGTGTGGCCGAGAGAGAGGAGTCTCTGAGGA 1140  
 DB 1081 CTTTCCAGGCTGAGAGCGAGCGGCCGAGAGAGTGTGGCCGAGAGAGAGGAGTCTCTGAGGA 1140

QY 1141 GCAGTGCAGGAGCTGTCAGAGGAGTACAGCAAACTGAAGGCCAGCTGTGAGAGTTCGGC 1200  
 DB 1141 GCAGTGCAGGAGCTGTCAGAGGAGTACAGCAAACTGAAGGCCAGCTGTGAGAGTTCGGC 1200

QY 1201 CAGGATCCAGGAGCATGAGAGGCGCATGTTCAGGTCTCTCCAGGCCCTTGGCCCCCGCC 1260  
 DB 1201 CAGGATCCAGGAGCATGAGAGGCGCATGTTCAGGTCTCTCCAGGCCCTTGGCCCCCGCC 1260

QY 1261 CCTTCCTTACCTTCTCTCTCTCCCTTGGCCCTGCGCCAGCAGAGAGGAGGCCCGCCCGAGGA 1320  
 DB 1261 CCTTCCTTACCTTCTCTCTCTCCCTTGGCCCTGCGCCAGCAGAGAGGAGGCCCGCCCGAGGA 1320

QY 1321 GCCACTGACTTCTGCTGTCCCAAGTGCAGATCAGGCCCTGTATATGGAACCTCTGCA 1380  
 DB 1321 GCCACTGACTTCTGCTGTCCCAAGTGCAGATCAGGCCCTGTATATGGAACCTCTGCA 1380

QY 1381 GATACATGTCTGAGTGCATTTGAGTGGCGCGCAGTGCAGAGGCCACTGTGCTGCCCGA 1440  
 DB 1381 GATACATGTCTGAGTGCATTTGAGTGGCGCGCAGTGCAGAGGCCACTGTGCTGCCCGA 1440





CC activity, are useful for the further definition of CD40-mediated  
 CC signaling pathways, and for manipulation of CD40-mediated cellular  
 CC responses. They also provide therapeutic agents for treating disorders of  
 CC the immune system, and inflammatory and cancer diseases. The present  
 CC sequence represents a DNA encoding the human NEMO polypeptide  
 XX  
 SQ Sequence 1994 BP; 429 A; 585 C; 633 G; 347 T; 0 U; 0 Other;

Query Match		100.0%; Score 1994; DB 10; Length 1994;
Best Local Similarity		100.0%; Pred. No. 0;
Matches 1994; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
QY	1	GGCAGAGATGCGCCCTTGTGATCCAGGTGGGAACTAAAGCCAGAGAAAGTGGAGCC 60
DB	1	GGCAGAGATGCGCCCTTGTGATCCAGGTGGGAACTAAAGCCAGAGAAAGTGGAGCC 60
QY	61	CGCGAGACTATCAATCCAGTCTTCCCTCACTCCCTGTGAAGCTTCCAGCATCATC 120
DB	61	CGCGAGACTATCAATCCAGTCTTCCCTCACTCCCTGTGAAGCTTCCAGCATCATC 120
QY	121	GAGGTCCCATCAGCCCTTCCCTGTGGATGAATAGGCACCTCTGAGAGCCAACTGTG 180
DB	121	GAGGTCCCATCAGCCCTTCCCTGTGGATGAATAGGCACCTCTGAGAGCCAACTGTG 180
QY	181	TGAGATGTGTGACGCCAGTGTGGCCCGGCAGCAGATCAGAGACGTACTGGGCGAAGAGTC 240
DB	181	TGAGATGTGTGACGCCAGTGTGGCCCGGCAGCAGATCAGAGACGTACTGGGCGAAGAGTC 240
QY	241	TCCTCTGGGGAAGCCAGCCATGCTGCACTGCTCTTCAAGAACAGGGCGCTCTTGAAGACCT 300
DB	241	TCCTCTGGGGAAGCCAGCCATGCTGCACTGCTCTTCAAGAACAGGGCGCTCTTGAAGACCT 300
QY	301	CCAGCGCTCCCTGGAGGAGAACTCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACCATG 360
DB	301	CCAGCGCTCCCTGGAGGAGAACTCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACCATG 360
QY	361	TCCTGGGAGAGCGCTGCGAGAGCTTCTGCAATTTCAAGCCAGCCAGAGGAGGAGAA 420
DB	361	TCCTGGGAGAGCGCTGCGAGAGCTTCTGCAATTTCAAGCCAGCCAGAGGAGGAGAA 420
QY	421	GTTCTCATGTGCAAGTTCAGAGAGCCAGGAACTGTGTGAGAGACTCGGCTTGAGAA 480
DB	421	GTTCTCATGTGCAAGTTCAGAGAGCCAGGAACTGTGTGAGAGACTCGGCTTGAGAA 480
QY	481	GCTTCATCTGAAGAGCAGAGAGCAGCTCTGCGGAGGTGGAGCACTCAAGAGATG 540
DB	481	GCTTCATCTGAAGAGCAGAGAGCAGCTCTGCGGAGGTGGAGCACTCAAGAGATG 540
QY	541	CCAGCAGCAGATGGGTGAGGACAAAGCCCTCTGTGAAAGCCAGGTGACGTCTTGTCTGG 600
DB	541	CCAGCAGCAGATGGGTGAGGACAAAGCCCTCTGTGAAAGCCAGGTGACGTCTTGTCTGG 600
QY	601	GGAGTGTGAGGAGCAGAGTGGTGTGAGGCTGCACTAAGGAAATGCCAGGCTCTGGA 660
DB	601	GGAGTGTGAGGAGCAGAGTGGTGTGAGGCTGCACTAAGGAAATGCCAGGCTCTGGA 660
QY	661	GGGTGGGCGCGGCGGCGCAGCAGCGCGGCGAGCTGGAGAGTGAGCGCGAGCGCT 720
DB	661	GGGTGGGCGCGGCGGCGCAGCAGCGCGGCGAGCTGGAGAGTGAGCGCGAGCGCT 720
QY	721	GCAGCAGCAGCAGCAGCTGAGTGGACCAAGCTGCGCATGCGAGGCGCAGAGCTGGAGGC 780
DB	721	GCAGCAGCAGCAGCAGCTGAGTGGACCAAGCTGCGCATGCGAGGCGCAGAGCTGGAGGC 780
QY	781	CGCGCTCCGCATGGAGCGCCAGCGCTTCCAGAGAGAGAGAAAGCTGGCCCACTTGA 840
DB	781	CGCGCTCCGCATGGAGCGCCAGCGCTTCCAGAGAGAGAGAAAGCTGGCCCACTTGA 840
QY	841	GCTGGCCTATCAGCTCTTCCAGAAATACCAACCAATCAAGCAGAGCGTGGTGGG 900
DB	841	GCTGGCCTATCAGCTCTTCCAGAAATACCAACCAATCAAGCAGAGCGTGGTGGG 900
QY	901	CAGTGAGCGGAAGCGAGGAATGAGCTGGAAGATCTCAAAACAGCAGCTCCAGCAGGCCGA 960

901	DB	CAGTGAGCGGAAGCGAGGAATGACGTGGAAGATCTCAAAACAGCAGCTCCAGCAGGCCGA 960
961	QY	GGAGCCCTGTGTGGCCAAACAGGAGGTGATCGATAAGCTGAAGAGGAGGCCGAGCAGCA 1020
961	DB	GGAGCCCTGTGTGGCCAAACAGGAGGTGATCGATAAGCTGAAGAGGAGGCCGAGCAGCA 1020
1021	QY	CAAGATTGTGATGAGAGACCGTTCCGGTGTGAAGGCCCCAGGCGGATATCTACAAGCGCA 1080
1021	DB	CAAGATTGTGATGAGAGACCGTTCCGGTGTGAAGGCCCCAGGCGGATATCTACAAGCGCA 1080
1081	QY	CTTCCAGGCTGAGAGCGAGCCCGGAGAGCTGCGCGAGAAAGAGAGCTCTCTGCAGGA 1140
1081	DB	CTTCCAGGCTGAGAGCGAGCCCGGAGAGCTGCGCGAGAAAGAGAGCTCTCTGCAGGA 1140
1141	QY	GCAGTGTGAGCAGCTGTGAGAGGAGTACAGCAAACTGAAGGCCAGCTGTGAGAGTGGC 1200
1141	DB	GCAGTGTGAGCAGCTGTGAGAGGAGTACAGCAAACTGAAGGCCAGCTGTGAGAGTGGC 1200
1201	QY	CAGGATCGAGGACATGAGGAGAGCGGCATGTGAGAGTCTCCAGAGCCCTTCCGCCCGC 1260
1201	DB	CAGGATCGAGGACATGAGGAGAGCGGCATGTGAGAGTCTCCAGAGCCCTTCCGCCCGC 1260
1261	QY	CCCTGCTACCT 1320
1261	DB	CCCTGCTACCT 1320
1321	QY	GCACCTGACT 1380
1321	DB	GCACCTGACT 1380
1381	QY	GATACATGTCATGAGTGCATTTAGTTCGCGCGGCGCAGTTCGCAAGGCCACTGCTGCCGA 1440
1381	DB	GATACATGTCATGAGTGCATTTAGTTCGCGCGGCGCAGTTCGCAAGGCCACTGCTGCCGA 1440
1441	QY	GGAGTGTGCGGAGCCGTGCGCT 1500
1441	DB	GGAGTGTGCGGAGCCGTGCGCT 1500
1501	QY	AGGGTGTGGTGGCCCAACTGGGATGCCACTGGAGAGCCCAAGGAGGAGCTGGCGCGGC 1560
1501	DB	AGGGTGTGGTGGCCCAACTGGGATGCCACTGGAGAGCCCAAGGAGGAGCTGGCGCGGC 1560
1561	QY	ACCTTACGCTTCAGCTGTGATCCGCTGCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1620
1561	DB	ACCTTACGCTTCAGCTGTGATCCGCTGCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1620
1621	QY	CAGGCTTGACTGCTGCT 1680
1621	DB	CAGGCTTGACTGCTGCT 1680
1681	QY	TAATCCCT 1740
1681	DB	TAATCCCT 1740
1741	QY	CAGGAGAGAACTGCTTCCCTCTGCGAGCTGGGTGCGAGCTCTCTCTCTCTCTCTCTCTCTCT 1800
1741	DB	CAGGAGAGAACTGCTTCCCTCTGCGAGCTGGGTGCGAGCTCTCTCTCTCTCTCTCTCTCTCT 1800
1801	QY	ACCGCCCGCGCGCTGTGCCCTTGGAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1860
1801	DB	ACCGCCCGCGCGCTGTGCCCTTGGAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1860
1861	QY	TTTTGGGCTGATGCTATTCATTTTGGAGCAGACCGATGTGTATTTTAAACAGTCACTA 1920
1861	DB	TTTTGGGCTGATGCTATTCATTTTGGAGCAGACCGATGTGTATTTTAAACAGTCACTA 1920
1921	QY	TTGATGGAACATTTGGTGTGTTTCCCATCTTTTGTGTACATAAATAAGTGGCATAGTAA 1980
1921	DB	TTGATGGAACATTTGGTGTGTTTCCCATCTTTTGTGTACATAAATAAGTGGCATAGTAA 1980
1981	QY	AAAAAAAAAAAAA 1994

Db 1981 AAAAAAAAAAAAAA 1994

RESULT 7

ABD20692

ID ABD20692 standard; DNA; 1994 BP.

AC ABD20692;

XX 29-JUL-2004 (first entry)

XX Human pulmonary and inflammatory target DNA #303.

DE Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;

XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;

KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;

KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;

KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;

KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;

KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;

XX pulmonary transplantation rejection; ds.

OS Homo sapiens.

XX W0200285309-A2.

PN 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIC-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shanabuddin S;

XX WPI; 2003-093058/08.

XX Pharmaceutical composition for treating asthma, has antisense

PT oligonucleotide containing less percentage of adenosine, targeted to

PT nucleic acids associated with lung airway or lung dysfunction, and

PT bronchodilating agent.

XX Claim 15; SEQ ID NO 12085; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,

CC comprising oligonucleotides, effective for alleviating

CC bronchoconstriction, respiratory tract inflammation, allergies and

CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,

CC surfactant depletion or hyposecretion, when administered to a mammal. The

CC oligonucleotides are derived from a gene encoding or regulating

CC expression of a target polypeptide associated with lung airway or lung

CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.

CC The invention also describes a kit, that comprises: (a) a delivery

CC device, in separate containers, (b) the oligonucleotides, (c)

CC instructions for adding a carrier and for use of the kit. The composition

CC of the invention has antiallergic, antiinflammatory, antiasthmatic,

CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a

CC beta-adrenergic agonist. The composition is useful for preventing or

CC treating a respiratory, lung or malignant disease. The administered

CC composition comprises oligo and is administered to reduce the production

CC or availability, or to increase the degradation of the target mRNA or to

CC reduce the amount of target polypeptide present in the lungs. The

CC pulmonary obstruction, and/or bronchoconstriction and/or lung

CC inflammation, allergies and/or surfactant hypoproduction are associated

CC with a disease or condition such as pulmonary vasoconstriction,

CC inflammation, allergies, asthma, impeded respiration, respiratory

CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary

CC hypertension, emphysema, chronic obstructive pulmonary disease, cancer,

CC transplantation rejection, pulmonary infections, bronchitis or cancer.

CC The reduced adenosine content of the anti-sense oligos corresponding to

CC thymidines present in the target RNA serves to prevent the breakdown of

CC the oligonucleotides into products that free adenosine into the system

CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to

CC prevent any unwanted effects due to it

XX

SQ Sequence 1994 BP; 429 A; 585 C; 633 G; 347 T; 0 U; 0 Other;

Query Match 100.0%; Score 1994; DB 11; Length 1994;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCACGAGCATGGCCCTTGTCATCCAGTGGGGAACTAAGCCCCAGAGAAAGTAGGACC 60

Db 1 GGCACGAGCATGGCCCTTGTCATCCAGTGGGGAACTAAGCCCCAGAGAAAGTAGGACC 60

QY 61 CCGCAGACTATCAATCCAGTCTCTTCCCTCTCACTCCCTGTGAAGCTCTCCAGCATCATC 120

Db 61 CCGCAGACTATCAATCCAGTCTCTTCCCTCTCACTCCCTGTGAAGCTCTCCAGCATCATC 120

QY 121 GAGTCCCATCAGCCCTTGGCTGTTGGATGAATAGGACCTCTGGAAGAGCAACTGTG 180

Db 121 GAGTCCCATCAGCCCTTGGCTGTTGGATGAATAGGACCTCTGGAAGAGCAACTGTG 180

QY 181 TGAGATGGTGCAGCCAGTGGTGGCCGCGCAGCAGATCAGGACCTACTGGGCGAGATC 240

Db 181 TGAGATGGTGCAGCCAGTGGTGGCCGCGCAGCAGATCAGGACCTACTGGGCGAGATC 240

QY 241 TCCTCTGGGGAAGCCAGCCATGCTGCACCTTCCAGAACAGGGCGCTCTCTGAGACCT 300

Db 241 TCCTCTGGGGAAGCCAGCCATGCTGCACCTTCCAGAACAGGGCGCTCTCTGAGACCT 300

QY 301 CCAGCGCTGCTGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACCATG 360

Db 301 CCAGCGCTGCTGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACCATG 360

QY 361 TCTGCGGGAGCGCTGGCAGGAGCTTCTGCAATTTCCAAAGCCAGAGGAGGAGAGGA 420

Db 361 TCTGCGGGAGCGCTGGCAGGAGCTTCTGCAATTTCCAAAGCCAGAGGAGGAGAGGA 420

QY 421 GTTCTCTATGTGCAAGTTCCAGAGGCGCAGGAACTGGTGGAGAGACTCGGCTCTGGGAA 480

Db 421 GTTCTCTATGTGCAAGTTCCAGAGGCGCAGGAACTGGTGGAGAGACTCGGCTCTGGGAA 480

QY 481 GCTCGATCTGAAGAGCGCAGAGGAGCTCTGCGGGAGGTGAGCACCTGAGAGATG 540

Db 481 GCTCGATCTGAAGAGCGCAGAGGAGCTCTGCGGGAGGTGAGCACCTGAGAGATG 540

QY 541 CCAGCAGCAGATGGCTGAGGACAAAGCCCTCTGTGAAAGCCAGGTGACGCTCTTGCTCGG 600

Db 541 CCAGCAGCAGATGGCTGAGGACAAAGCCCTCTGTGAAAGCCAGGTGACGCTCTTGCTCGG 600

QY 601 GGAGCTGCGAGGAGCGCAGAGTGGCTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGGA 660

Db 601 GGAGCTGCGAGGAGCGCAGAGTGGCTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGGA 660

QY 661 GGTGCGGGCCCGGGCGCCAGCGAGCAGCGCGGCGAGCTGGAGAGTCAGCGCCAGCGCT 720

Db 661 GGTGCGGGCCCGGGCGCCAGCGAGCAGCGCGGCGAGCTGGAGAGTCAGCGCCAGCGCT 720

QY 721 GCAGCAGCAGCAGCGCTGCGAGTGGACCAAGCTGCGCATGTCAGGGCCAGAGCGTGGAGGC 780

Db 721 GCAGCAGCAGCAGCGCTGCGAGTGGACCAAGCTGCGCATGTCAGGGCCAGAGCGTGGAGGC 780

QY 781 CCGGCTCCGCATGGAGCGCCAGCGCCCTCGGAGGAGAGAGAAAGTGGCCAGTGGCA 840

Db 781 CCGGCTCCGCATGGAGCGCCAGCGCCCTCGGAGGAGAGAGAAAGTGGCCAGTGGCA 840

QY 841 GTTGGCTATACCAAGCTCTTCCAAAGAAATACGACACCATCAAGAGCAGCGCTGGTGGG 900

Db 841 GTTGGCTATACCAAGCTCTTCCAAAGAAATACGACACCATCAAGAGCAGCGCTGGTGGG 900

QY 901 CAGTGGCGGAGCGAGGAGTGCAGTGGAAATCTCAAAACAGCAGCTCCAGAGGCCGA 960

Db 901 CAGTGGCGGAGCGAGGAGTGCAGTGGAAATCTCAAAACAGCAGCTCCAGAGGCCGA 960

Qy	961	GGAGGCCCTCGTGGCCAAA	CAGGAGGTGATGCTGA	TAACTGAAGAGAGGCGCGAGCAGCA	1021
Db	961	GGAGGCCCTCGTGGCCAAA	CAGGAGGTGATGCTGA	TAACTGAAGAGAGGCGCGAGCAGCA	1020
Qy	1021	CAAGATTGTGATGAGACCGTT	TCGGTGTGTAAGGCCACG	CGCGATATCTACAAAGGCGGA	1080
Db	1021	CAAGATTGTGATGAGACCGTT	TCGGTGTGTAAGGCCACG	CGCGATATCTACAAAGGCGGA	1080
Qy	1081	CTTCCAGGCTGAGAGCGAGCC	CGGGAGAAAGCTGGCCGAGA	GAAGAGAGCTCTCTGACAGGA	1140
Db	1081	CTTCCAGGCTGAGAGCGAGCC	CGGGAGAAAGCTGGCCGAGA	GAAGAGAGCTCTCTGACAGGA	1140
Qy	1141	GCAGCTGGAGCAGCTGAGAGG	AGATACGAAACTGAAGGCC	CAGCTGTGAGAGTCCCTGACGA	1200
Db	1141	GCAGCTGGAGCAGCTGAGAGG	AGATACGAAACTGAAGGCC	CAGCTGTGAGAGTCCCTGACGA	1200
Qy	1201	CAGGATCGAGGACATGAGGA	AGCGGCATGTGAGGTCTCC	AGGCCCTTTGGCCCCCGC	1260
Db	1201	CAGGATCGAGGACATGAGGA	AGCGGCATGTGAGGTCTCC	AGGCCCTTTGGCCCCCGC	1260
Qy	1261	CCCTGCGCTACCTCTCTCTC	TCCCTTGGCCCTGCCCAGC	CAGAGGAGGAGCCCCCGCAGGA	1320
Db	1261	CCCTGCGCTACCTCTCTCTC	TCCCTTGGCCCTGCCCAGC	CAGAGGAGGAGCCCCCGCAGGA	1320
Qy	1321	GCCACCTGACTTCTGCTGT	CCCAAGTGCCAGTATCAGG	CCCCCTGATGACACCCCTGCA	1380
Db	1321	GCCACCTGACTTCTGCTGT	CCCAAGTGCCAGTATCAGG	CCCCCTGATGACACCCCTGCA	1380
Qy	1381	GATACATGTATGAGAGTGCA	TTGAGTAGGGCGGCGCAGT	GCAAGGCCACCTGCTGCCCGA	1440
Db	1381	GATACATGTATGAGAGTGCA	TTGAGTAGGGCGGCGCAGT	GCAAGGCCACCTGCTGCCCGA	1440
Qy	1441	GGAGCTGCCGGGACCTGCA	GTCTGCGCTTTCTCTCCG	CCCTGCTAGCCAGGATGA	1500
Db	1441	GGAGCTGCCGGGACCTGCA	GTCTGCGCTTTCTCTCCG	CCCTGCTAGCCAGGATGA	1500
Qy	1501	AGGCTGGGTGGCCCAACT	GGGATGCCACTTGGAGCCC	ACCCAGAGAGTGCGCGCGC	1560
Db	1501	AGGCTGGGTGGCCCAACT	GGGATGCCACTTGGAGCCC	ACCCAGAGAGTGCGCGCGC	1560
Qy	1561	ACCTTAGCTTCAGCTGTGAT	TCGGCTGGTCCCTCTTTT	GGGGTAGATCGGGCCCCGAT	1620
Db	1561	ACCTTAGCTTCAGCTGTGAT	TCGGCTGGTCCCTCTTTT	GGGGTAGATCGGGCCCCGAT	1620
Qy	1621	CAGGCTTGACTCGCTGCT	TTTTTTGTTCCCTTCTGCT	GTCTCGAACCACTTGCTCGGGC	1680
Db	1621	CAGGCTTGACTCGCTGCT	TTTTTTGTTCCCTTCTGCT	GTCTCGAACCACTTGCTCGGGC	1680
Qy	1681	TAATCCCTCCCTCTTCTCCA	CCCGGCACTGGGGAAGTCA	AGAAATGGGGCTCTGGGGCTCT	1740
Db	1681	TAATCCCTCCCTCTTCTCCA	CCCGGCACTGGGGAAGTCA	AGAAATGGGGCTCTGGGGCTCT	1740
Qy	1741	CAGGGAGAACTGTCTTCCCT	TGGCAGAGCTGGGTGGCAG	CTTCTCCCAACCGGACACCG	1800
Db	1741	CAGGGAGAACTGTCTTCCCT	TGGCAGAGCTGGGTGGCAG	CTTCTCCCAACCGGACACCG	1800
Qy	1801	ACCCGCGCGCGCTGTCGCT	TGGGAGTGCTGCCCTCTTAC	CATGCAACCGGTGCTCTCC	1860
Db	1801	ACCCGCGCGCGCTGTCGCT	TGGGAGTGCTGCCCTCTTAC	CATGCAACCGGTGCTCTCC	1860
Qy	1861	TTTTTGGGCTGATCTATTCC	ATTATTTTGCAGCCAGACCG	ATGTGATTTAACCACTCACTA	1920
Db	1861	TTTTTGGGCTGATCTATTCC	ATTATTTTGCAGCCAGACCG	ATGTGATTTAACCACTCACTA	1920
Qy	1921	TTGATGGACATTTGGGTGTT	TTCCTCTTTTGTACCA	TAAATAATGCGCATGTAATA	1980
Db	1921	TTGATGGACATTTGGGTGTT	TTCCTCTTTTGTACCA	TAAATAATGCGCATGTAATA	1980
Qy	1981	AAAAAAAAAAAAAAAA	1994		
Db	1981	AAAAAAAAAAAAAAAA	1994		

XX	RESULT 8
XX	AAA35028
XX	ID AAA35028 standard; DNA; 8631 BP.
XX	AAA35028;
XX	28-JUL-2000 (first entry)
XX	Human adenosine receptor related polynucleotide SEQ ID NO:2717.
XX	Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW	phosphorothioate; impaired respiration; inflammation; allergy;
KW	allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW	antiallergic; ischaemic condition; cytostatic; analgesic; impaired airway;
KW	lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW	respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW	pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW	cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX	
OS	Homo sapiens.
XX	
XX	WO200009525-A2.
XX	24-FEB-2000.
PD	
XX	
XX	03-AUG-1999; 99WO-US017712.
PF	
XX	
XX	03-AUG-1998; 98US-0095212P.
PR	
XX	(UYEC-) UNIV EAST CAROLINA.
PA	
XX	
XX	Nyce JW;
PI	
XX	
DR	WPI; 2000-205971/18.
XX	
PT	New antisense oligonucleotides useful for treating e.g. pulmonary
PT	vasoconstriction, inflammation, allergies, asthma, hypertension,
PT	bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT	cancers.
XX	
XX	Disclosure; Page 969-971; 1343pp; English.
PS	
XX	
CC	The present invention describes a new composition comprising an antisense
CC	oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC	nucleic acids involved in bronchoconstriction, allergies, and/or
CC	inflammation. The ON can have antiinflammatory, antiallergic,
CC	antiasthmatic, cytostatic and analgesic activities. The compositions are
CC	useful for the treatment of diseases associated with inflammation,
CC	impaired airways, including lung disease and diseases whose secondary
CC	effects afflict the lungs of a subject. They can be used for treating
CC	e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC	impaired respiration, respiratory distress syndrome, pain, cystic
CC	fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC	pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC	carcinomas, and cancers which may metastasise to the lungs, including
CC	breast and prostate cancer. The reduction of the adenosine content of the
CC	ONS reduces side effects. The A-containing ONS break down with the
CC	release of deoxyadenosine which activates adenosine receptors causing
CC	bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC	nucleotide sequences given in the sequence listing from the present
CC	invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC	sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC	from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC	AAA33992) are specifically claimed ONS from the present invention. N.B.
CC	sequences given in the disclosure of the present invention do not match
CC	up with their corresponding SEQ ID NO: sequences given in the sequence
CC	listing
XX	
XX	Sequence 8631 BP; 2280 A; 2050 C; 2270 G; 2031 T; 0 U; 0 Other;
XX	
XX	Query Match 100.0%; Score 1994; DB 3; Length 8631;
XX	Best Local Similarity 100.0%; Pred. No. 0;

Matches 1994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	GGCAGCAGATGACCCCTTGTGATCCAGGTGGGAACTAAGCCCCAGAGAGTGAAGACC	60
Db	6638	GGCAGCAGATGACCCCTTGTGATCCAGGTGGGAACTAAGCCCCAGAGAGTGAAGACC	6697
QY	61	CCGACAGATATCAATCCCAAGTCTTTCCTCCCTCACTCCCTGTGAAGCTCTCCAGCATATC	120
Db	6698	CCGACAGATATCAATCCCAAGTCTTTCCTCCCTCACTCCCTGTGAAGCTCTCCAGCATATC	6757
QY	121	GAGTCCCATCAGCCCTTGGCCCTGTGGATGAATAGGCACTCTCGAAGACCACTGTG	180
Db	6758	GAGTCCCATCAGCCCTTGGCCCTGTGGATGAATAGGCACTCTCGAAGACCACTGTG	6817
QY	181	TGAGATGGTGCAGCCAGGTGGCCCGCAGCAGATCAGGACGTACTTGGGGAGAGTC	240
Db	6818	TGAGATGGTGCAGCCAGGTGGCCCGCAGCAGATCAGGACGTACTTGGGGAGAGTC	6877
QY	241	TCCTCTGGGAAAGCCAGCCATGCTGCACCTGCTTCAGAAACAGGGCGCTCCTGAGACCT	300
Db	6878	TCCTCTGGGAAAGCCAGCCATGCTGCACCTGCTTCAGAAACAGGGCGCTCCTGAGACCT	6937
QY	301	CCAGCCCTGCTGGAGGAGAAATCAAGAGCTCCGAGATGCCATTCGGCAGAGCAACAGAT	360
Db	6938	CCAGCCCTGCTGGAGGAGAAATCAAGAGCTCCGAGATGCCATTCGGCAGAGCAACAGAT	6997
QY	361	TCGCGGAGCGCTGCGAGAGCTTCTGCATTTCCAGCCAGCCAGCCAGGAGGAGAGGA	420
Db	6998	TCGCGGAGCGCTGCGAGAGCTTCTGCATTTCCAGCCAGCCAGCCAGGAGGAGAGGA	7057
QY	421	GTTCTCTATGTGCAAGTTCCAGAGGCGCAGGAAACTGGTGAGAGACTCGGCCCTGGAGAA	480
Db	7058	GTTCTCTATGTGCAAGTTCCAGAGGCGCAGGAAACTGGTGAGAGACTCGGCCCTGGAGAA	7117
QY	481	GCTCGATCTGAAGAGCAGAGGAGAGCTCTGCGGAGGTGAGACACTTGAAGAGATG	540
Db	7118	GCTCGATCTGAAGAGCAGAGGAGAGCTCTGCGGAGGTGAGACACTTGAAGAGATG	7177
QY	541	CCAGCAGCAGATGGCTGAGGACAGGCTCTGTGAAGCCAGGTGACGCTTGTCTCGG	600
Db	7178	CCAGCAGCAGATGGCTGAGGACAGGCTCTGTGAAGCCAGGTGACGCTTGTCTCGG	7237
QY	601	GGAGCTGACGAGAGCCAGAGTCGCTTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGGA	660
Db	7238	GGAGCTGACGAGAGCCAGAGTCGCTTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGGA	7297
QY	661	GGGTGGGCGCGCGCGCCAGCAGCAGCGCGGAGCTGAGAGTGAAGCGGAGGCGCT	720
Db	7298	GGGTGGGCGCGCGCGCCAGCAGCAGCGCGGAGCTGAGAGTGAAGCGGAGGCGCT	7357
QY	721	GCAGCAGCAGCAGCAGCTGCAAGTGGACCCAGCTGCGCATGCAGGGCCAGAGCGTGGAGGC	780
Db	7358	GCAGCAGCAGCAGCAGCTGCAAGTGGAGTGGACCTGCGCATGCAGGGCCAGAGCGTGGAGGC	7417
QY	781	CGCGCTCCGATGAGAGCCAGCGCGCTCGGAGAGAGAGGAACTGGCCCACTTGCA	840
Db	7418	CGCGCTCCGATGAGAGCCAGCGCGCTCGGAGAGAGAGGAACTGGCCCACTTGCA	7477
QY	841	GGTGGCCCTATCACCAGCTCTTCAGAGATACGACCAATCAAGAGCAGCGTGGTGGG	900
Db	7478	GGTGGCCCTATCACCAGCTCTTCAGAGATACGACCAATCAAGAGCAGCGTGGTGGG	7537
QY	901	CAGTGAGCGGAGCAGGAGATGCAAGTGGAAAGTCTCAACAGCAGCTCCAGCAGGCGCA	960
Db	7538	CAGTGAGCGGAGCAGGAGATGCAAGTGGAAAGTCTCAACAGCAGCTCCAGCAGGCGCA	7597
QY	961	GGAGCCCTGTGGCCAAACAGAGGAGTGAATGATAGCTGAAGAGAGAGCCCGAGCAGCA	1020
Db	7598	GGAGCCCTGTGGCCAAACAGAGGAGTGAATGATAGCTGAAGAGAGAGCCCGAGCAGCA	7657
QY	1021	CAAGATTTGTATGAGACCGTTCGCGTGTGAAGGCCAGCGGATATCTACAGGCGGA	1080
Db	7658	CAAGATTTGTATGAGACCGTTCGCGTGTGAAGGCCAGCGGATATCTACAGGCGGA	7717

QY	1081	CTTCCAGGCTGAGAGGAGGAGCCCGGAGAAAGCTGGCCGAGAAAGAGAGTCTCTTCAGGA	1140
Db	7718	CTTCCAGGCTGAGAGGAGGAGCCCGGAGAAAGCTGGCCGAGAAAGAGAGTCTCTTCAGGA	7777
QY	1141	GCAGCTGAGCAGCTGACAGAGGAGTACAGAACTGAGAGCCAGCTCTCAGGAGTCCGC	1200
Db	7778	GCAGCTGAGCAGCTGACAGAGGAGTACAGAACTGAGAGCCAGCTCTCAGGAGTCCGC	7837
QY	1201	CAGGATCGAGGACATGAGGAAAGCGGCATGTCCAGGCTCTCCAGGCCCCCTTGGCCCCCGC	1260
Db	7838	CAGGATCGAGGACATGAGGAAAGCGGCATGTCCAGGCTCTCCAGGCCCCCTTGGCCCCCGC	7897
QY	1261	CCCTGCTACTCTCTCTCTCCCTGGCCCTGCCCCAGCAGAGGAGAGCCCCCCCCGAGA	1320
Db	7898	CCCTGCTACTCTCTCTCTCCCTGGCCCTGCCCCAGCAGAGGAGAGCCCCCCCCGAGA	7957
QY	1321	GCACCTGACTTCTGCTGCTCCCAAGTCCAGTATCAGGCCCTCATATGACACCCCTGCA	1380
Db	7958	GCACCTGACTTCTGCTGCTCCCAAGTCCAGTATCAGGCCCTCATATGACACCCCTGCA	8017
QY	1381	GATACATGTTCATGGAGTGCATTGAGTAGGCGCGGCCAGTGCAGGCCACTGCCTGCCCCGA	1440
Db	8018	GATACATGTTCATGGAGTGCATTGAGTAGGCGCGGCCAGTGCAGGCCACTGCCTGCCCCGA	8077
QY	1441	GGAGTGGCCCGGAGCAGTGCAGTCTGGCTTCTCTCCGCTGCTCTAGCCAGGATGA	1500
Db	8078	GGAGTGGCCCGGAGCAGTGCAGTCTGGCTTCTCTCCGCTGCTCTAGCCAGGATGA	8137
QY	1501	AGGGCTGGGTGGCCACAACTGGGATGCCACTGGAGCCCCCAGCAGAGCTGGCGCGGC	1560
Db	8138	AGGGCTGGGTGGCCACAACTGGGATGCCACTGGAGCCCCCAGCAGAGCTGGCGCGGC	8197
QY	1561	ACCTTACGCTTACGCTGTTGATCCGCTGCTCTTTTGGGTAGATGGCGGCCCGAT	1620
Db	8198	ACCTTACGCTTACGCTGTTGATCCGCTGCTCTTTTGGGTAGATGGCGGCCCGAT	8257
QY	1621	CAGGCTGACTCGCTGCTCTTTTGTCTCTGCTGCTCGAACCACTTGGCTCGGGC	1680
Db	8258	CAGGCTGACTCGCTGCTCTTTTGTCTCTGCTGCTCGAACCACTTGGCTCGGGC	8317
QY	1681	TATATCCCTCCCTCTCTCCACCCGACCTGGGGAAGTCAAGAAATGGGGCTGGGGTCT	1740
Db	8318	TATATCCCTCCCTCTCTCCACCCGACCTGGGGAAGTCAAGAAATGGGGCTGGGGTCT	8377
QY	1741	CAGGAGAACTGCTTCCCTTGGCAGAGCTGGGTGGCAGCTTCTTCCCTCCACCGACACCG	1800
Db	8378	CAGGAGAACTGCTTCCCTTGGCAGAGCTGGGTGGCAGCTTCTTCCCTCCACCGACACCG	8437
QY	1801	ACCCGCCCGCGCTGCTGGAGTGGCTTACCATTTTTCAGCCAGACCGATGTATTTAAACCACTA	1860
Db	8438	ACCCGCCCGCGCTGCTGGAGTGGCTTACCATTTTTCAGCCAGACCGATGTATTTAAACCACTA	8497
QY	1861	TTTTGGGCTGCATGCTATTTCCATTTTTCAGCCAGACCGATGTATTTAAACCACTA	1920
Db	8498	TTTTGGGCTGCATGCTATTTCCATTTTTCAGCCAGACCGATGTATTTAAACCACTA	8557
QY	1921	TTGATGGCAATTTGGGTGTTTCCCATCTTTTGTTCACATAAATATAGTACTAGTAAAA	1980
Db	8558	TTGATGGCAATTTGGGTGTTTCCCATCTTTTGTTCACATAAATATAGTACTAGTAAAA	8617
QY	1981	AAAAAAAAAAAAAA 1994	
Db	8618	AAAAAAAAAAAAAA 8631	

RESULT 9  
AAF21150  
ID AAF21150 standard; DNA; 8631 Bp.  
XX  
AC AAF21150;  
XX  
DT 14-MAR-2001 (first entry)



XX	Human low adenosine antisense oligonucleotide related sequence #2717.	QY	1	GGCAGAGATGAGGCGCTTGTGATCCAGGTGGGAACTAAGGCCAGAGAAAGTGGAGCC	60
DE		DB	6638	GGCAGAGATGAGGCGCTTGTGATCCAGGTGGGAACTAAGGCCAGAGAAAGTGGAGCC	6697
KW	Low adenosine antisense oligonucleotide; phosphorothioate; allergy;	QY	61	CGCAGAGATGAGGCGCTTGTGATCCAGGTGGGAACTAAGGCCAGAGAAAGTGGAGCC	120
KW	human; airway disorder; bronchoconstriction; lung inflammation;	DB	6698	CGCAGAGATGAGGCGCTTGTGATCCAGGTGGGAACTAAGGCCAGAGAAAGTGGAGCC	6757
KW	surfactant depletion; respiratory bronchodilator; anti-inflammatory;	QY	121	GAGGTCCCATCAGGCGCTTGTGATCCAGGTGGGAACTAAGGCCAGAGAAAGTGGAGCC	180
KW	immunosuppressive; antiasthmatic; analgesic; hypotensive; cytosolic;	DB	6758	GAGGTCCCATCAGGCGCTTGTGATCCAGGTGGGAACTAAGGCCAGAGAAAGTGGAGCC	6817
KW	respiratory obstruction; pulmonary obstruction; impeded respiration;	QY	181	TCAGATGCTGAGGCGCTTGTGATCCAGGTGGGAACTAAGGCCAGAGAAAGTGGAGCC	240
KW	surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;	DB	6818	TCAGATGCTGAGGCGCTTGTGATCCAGGTGGGAACTAAGGCCAGAGAAAGTGGAGCC	6877
KW	respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;	QY	241	TCCTCTGGGAAAGCCAGGCGCTTGTGATCCAGGTGGGAACTAAGGCCAGAGAAAGTGGAGCC	300
KW	pulmonary hypertension; emphysema; pulmonary transplantation rejection;	DB	6878	TCCTCTGGGAAAGCCAGGCGCTTGTGATCCAGGTGGGAACTAAGGCCAGAGAAAGTGGAGCC	6937
KW	chronic obstructive pulmonary disease; pulmonary infection; bronchitis;	QY	301	CCAGCGCTGCTGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGCGCAGAGCAACAGAT	360
OS	Canis sapiens.	DB	6938	CCAGCGCTGCTGGAGGAGAAATCAAGAGCTCCGAGATGCCATCCGCGCAGAGCAACAGAT	6997
XX		QY	361	TCTGCGGAGCGCTGCGAGGAGCTTCTGCAATTTTCAAGCCAGAGAGAGAGAGAGAA	420
XX	WO200062736-A2.	DB	6998	TCTGCGGAGCGCTGCGAGGAGCTTCTGCAATTTTCAAGCCAGAGAGAGAGAGAGAA	7057
XX	26-OCT-2000.	QY	421	GTTCTCATGTGCAAGTTTCCAGGAGGCGCAGGAACTGTTGAGAGAGACTCGGCTCGAGAA	480
XX	24-MAR-2000; 2000WO-US008020.	DB	7058	GTTCTCATGTGCAAGTTTCCAGGAGGCGCAGGAACTGTTGAGAGAGACTCGGCTCGAGAA	7117
XX	06-APR-1999; 99US-0127958P.	QY	481	GCTCGATCTGAGGAGGCGCAGGAGGCGCTGCGGAGGAGTGGAGCACTTCAAGAGAGT	540
XX	(UYEC-) UNIV EAST CAROLINA.	DB	7118	GCTCGATCTGAGGAGGCGCAGGAGGCGCTGCGGAGGAGTGGAGCACTTCAAGAGAGT	7177
XX	(NYCE/) NYCE J W.	QY	541	CCAGCAGCAGATGGCTGAGGAGCAAGGCGCTCTGTGAAAGCCAGAGTCCCTTCTGTCGG	600
PI	Nyce JW;	DB	7178	CCAGCAGCAGATGGCTGAGGAGCAAGGCGCTCTGTGAAAGCCAGAGTCCCTTCTGTCGG	7237
XX	WPI; 2000-679539/66.	QY	601	GGAGTGCAGGAGAGCCAGAGTGGTTCGAGGCTGCCACTAAGAAATGCGAGTCTTGA	660
XX	Low adenosine (A) content antisense oligonucleotides which do not trigger	DB	7238	GGAGTGCAGGAGAGCCAGAGTGGTTCGAGGCTGCCACTAAGAAATGCGAGTCTTGA	7297
XX	adenosine receptors during metabolism, useful e.g. for treating cancers	QY	661	GGGTCCG	720
XX	and respiratory obstructions.	DB	7298	GGGTCCG	7357
PS	Disclosure; Page 1046-1048; 1592pp; English.	QY	721	GCAGCAGCAGCAGCAGCGTGCAGGTGAGCAAGTCCGCGCATGCGAGGCGCGAGCGTGGAGC	780
CC	The present invention describes low adenosine (A) content antisense	DB	7358	GCAGCAGCAGCAGCAGCGTGCAGGTGAGCAAGTCCGCGCATGCGAGGCGCGAGCGTGGAGC	7417
CC	oligonucleotides and compositions (I) comprising them. In the antisense	QY	781	CGCGTCCGCGCATGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	840
CC	oligonucleotides the A is replaced by a 'Universal' or alternative base.	DB	7418	CGCGTCCGCGCATGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	7477
CC	(I) can have respiratory, bronchodilator, anti-inflammatory, analgesic,	QY	841	GGTCCGCTTATCAGCAGCTTCTCCAGAGATAGCAACCAACCATCAAGAGCAGCGTGGTGG	900
CC	immunosuppressive, antiasthmatic, hypotensive and cytosolic activities.	DB	7478	GGTCCGCTTATCAGCAGCTTCTCCAGAGATAGCAACCAACCATCAAGAGCAGCGTGGTGG	9537
CC	The antisense oligonucleotides and (I) can be used to down-regulate the	QY	901	CAGTCCG	960
CC	expression and/or activity of target polypeptides associated with	DB	7538	CAGTCCG	9597
CC	lung/respiratory disorders and malignancies, such as stimulating and	QY	961	GGAGGCGCTTGTGGCG	1020
CC	activating peptide factors and transmitters, transcription factors,	DB	7598	GGAGGCGCTTGTGGCG	7657
CC	immunoglobulins and antibodies, antibody receptors, cytokines and	QY	1021	CAAGATTTGTGAGGAGCGGTTCCGCGTCTGAGGCGCGCGCGCGCGCGCGCGCGCGCG	1080
CC	chemokines, endogenously produced specific and non-specific enzymes,	DB	7658	CAAGATTTGTGAGGAGCGGTTCCGCGTCTGAGGCGCGCGCGCGCGCGCGCGCGCGCG	7717
CC	binding proteins, adhesion molecules and their receptors, cytokine and	QY	1081	CTTCCAGGCTGAGAGGCG	1140
CC	chemokine receptors, adenosine receptors, bradykinin receptors, central				
CC	nervous system (CNS) and peripheral nervous and non-nervous system				
CC	receptors, CNS and peripheral nervous and non-nervous system peptide				
CC	transmitters, defensins, growth factors, vasoactive peptides and				
CC	receptors, binding proteins and malignancy associated proteins. The				
CC	antisense oligonucleotides may be used in this way to treat disorders				
CC	including respiratory obstruction (especially pulmonary obstruction				
CC	and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or				
CC	surfactant hypoproduction which are associated with a disease or				
CC	condition selected from pulmonary vasoconstriction, inflammation,				
CC	allergies, asthma, impeded respiration, respiratory distress syndrome				
CC	(RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary				
CC	hypertension, emphysema, chronic obstructive pulmonary disease (COPD),				
CC	pulmonary transplantation rejection, pulmonary infections, bronchitis,				
CC	and/or cancer. AAF18434 to AAF21543 represent human polynucleotide				
CC	fragments and antisense oligonucleotides used in the exemplification of				
CC	the present invention				
XX					
XX	Sequence 8631 BP; 2280 A; 2050 C; 2270 G; 2031 T; 0 U; 0 Other;				
XX	Query Match 100.0%; Score 1994; DB 3; Length 8631;				
XX	Best Local Similarity 100.0%; Pred. No. 0;				
XX	Matches 1994; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				



Db 6818 TGAGATGGTGCAGCCCAAGTGGTGGCCCGCAGCAGATCAGGACGTACTGGGCGAAGAGTC 6877  
Qy 241 TCCTCTGGGGAGCCAGCAGCATGCTGCACCTGCTTCAGAACAGGGCGCTCCTGAGACCTT 300  
Db 6878 TCCTCTGGGGAGCCAGCAGCATGCTGCACCTGCTTCAGAACAGGGCGCTCCTGAGACCTT 6937  
Qy 301 CCAGCGCTCCCTGGAGGAGAAACAAGAGCTCCGAGATGCCATCCGCGCAGCAACCCAGAT 360  
Db 6938 CCAGCGCTCCCTGGAGGAGAAACAAGAGCTCCGAGATGCCATCCGCGCAGCAACCCAGAT 6997  
Qy 361 TCTGCGGGAGCGCTGCGAGAGCTTCTGCAATTCGAAGCCAGCAGCAGAGGAGGAGAGGA 420  
Db 6998 TCTGCGGGAGCGCTGCGAGAGCTTCTGCAATTCGAAGCCAGCAGCAGAGGAGGAGAGGA 7057  
Qy 421 GTTCTCTATGTGCAAGTTCACAGAGCCAGGAAACTGTGTGGAGAGACTCGGCTTGAGAA 480  
Db 7058 GTTCTCTATGTGCAAGTTCACAGAGCCAGGAAACTGTGTGGAGAGACTCGGCTTGAGAA 7117  
Qy 481 GCTCGATCTGAAGAGCCAGAGCAGGCTCTGCGGGAGGTGGAGCACTTGAAGAGATG 540  
Db 7118 GCTCGATCTGAAGAGCCAGAGCAGGCTCTGCGGGAGGTGGAGCACTTGAAGAGATG 7177  
Qy 541 CCAGCAGCAGATGGCTGAGGAAACAAGCCCTCTGTGAAGCCAGGTGAACCTCTTGTCTGG 600  
Db 7178 CCAGCAGCAGATGGCTGAGGAAACAAGCCCTCTGTGAAGCCAGGTGAACCTCTTGTCTGG 7237  
Qy 601 GGAGCTGCAAGGAGAGCCAGAGTCGCTTGAGAGCTGCCACTAAGGAATGCCAGGCTCTGGA 660  
Db 7238 GGAGCTGCAAGGAGAGCCAGAGTCGCTTGAGAGCTGCCACTAAGGAATGCCAGGCTCTGGA 7297  
Qy 661 GGGTCCGGCCCGGGCCAGCAGCAGCGCGGCGCAGCTGGAGAGTGAAGCGGAGCGCT 720  
Db 7298 GGGTCCGGCCCGGGCCAGCAGCAGCGCGGCGCAGCTGGAGAGTGAAGCGGAGCGCT 7357  
Qy 721 GCAGCAGCAGCAGCGCTGAGGTGACAGCTGCGCATGCAAGGCGCAGAGCGTGGAGGC 780  
Db 7358 GCAGCAGCAGCAGCGCTGAGGTGACAGCTGCGCATGCAAGGCGCAGAGCGTGGAGGC 7417  
Qy 781 CCGCTCCCGCATGAGCGCCAGCGCCCTCGAGAGAGAGAGAGCTGGCCCGAGTTGCA 840  
Db 7418 CCGCTCCCGCATGAGCGCCAGCGCCCTCGAGAGAGAGAGAGCTGGCCCGAGTTGCA 7477  
Qy 841 GGTGGCCTATACCAAGCTCTTCCAGAAATACGACCAACCAATCAAGAGCAGCGTGGTGG 900  
Db 7478 GGTGGCCTATACCAAGCTCTTCCAGAAATACGACCAACCAATCAAGAGCAGCGTGGTGG 7537  
Qy 901 CAGTGAAGCGAAGCGAGGAATGAGCTGGAAGATCTCAAAACAGCAGCTCCAGAGGCCGA 960  
Db 7538 CAGTGAAGCGAAGCGAGGAATGAGCTGGAAGATCTCAAAACAGCAGCTCCAGAGGCCGA 7597  
Qy 961 GGAGGCCCTGGTGGCCAAACAGAGGATGATCGATAGCTGAAGGAGGAGGCCGAGCAGCA 1020  
Db 7598 GGAGGCCCTGGTGGCCAAACAGAGGATGATCGATAGCTGAAGGAGGAGGCCGAGCAGCA 7657  
Qy 1021 CAAGATTGTGTGAGAGACCGTTCCGGTGTGAAGCCCGAGCGGATATCTCAAGGCGGA 1080  
Db 7658 CAAGATTGTGTGAGAGACCGTTCCGGTGTGAAGCCCGAGCGGATATCTCAAGGCGGA 7717  
Qy 1081 CTTTCAGGCTGAGAGCAGGCCCGGAGAAAGTGGCCGAGAAAGAGAGCTCCTGACAGA 1140  
Db 7718 CTTTCAGGCTGAGAGCAGGCCCGGAGAAAGTGGCCGAGAAAGAGAGCTCCTGACAGA 7777  
Qy 1141 GCAGCTGGAGCAGCTGACAGAGGAGTACAGCAAACTGAGGCCAGCTGTACAGAGTCCGC 1200  
Db 7778 GCAGCTGGAGCAGCTGACAGAGGAGTACAGCAAACTGAGGCCAGCTGTACAGAGTCCGC 7837  
Qy 1201 CAGGATTCAGAGGACATGAGGAAGCGGCATGTCCAGGTCTCCAGGCCCTTCCGCCCGCC 1260  
Db 7838 CAGGATTCAGAGGACATGAGGAAGCGGCATGTCCAGGTCTCCAGGCCCTTCCGCCCGCC 7897  
Qy 1261 CCTGCTGCTACCTCTCTCTCCCTGGCCCTGCGCCAGCAGAGAGAGGCCCGCCGAGGA 1320  
Db 7898 CCTGCTGCTACCTCTCTCTCTCCCTGGCCCTGCGCCAGCAGAGAGAGGCCCGCCGAGGA 7957

Qy 1321 GCCACCTGACTTCTGCTGTCCCAAGTGCAGTATCAGGCCCCCTGATATGACACACCTGCA 1380  
Db 7958 GCCACCTGACTTCTGCTGTCCCAAGTGCAGTATCAGGCCCCCTGATATGACACACCTGCA 8017  
Qy 1381 GATACATGTCATGGAGTGCATTGAGTAGGGCCGGCCAGTGCAGAGGCACTTGCTGCCCCGA 1440  
Db 8018 GATACATGTCATGGAGTGCATTGAGTAGGGCCGGCCAGTGCAGAGGCACTTGCTGCCCCGA 8077  
Qy 1441 GGACGTGCCCGGAGCCGTGCAGTCTGCGCTTTCCTCTCCGGCTGCTGAGCCAGGATGA 1500  
Db 8078 GGACGTGCCCGGAGCCGTGCAGTCTGCGCTTTCCTCTCCGGCTGCTGAGCCAGGATGA 8137  
Qy 1501 AGGGCTGGGTGGCCCAACTGGGATGCCACTGGAGCCCCACCCAGGAGCTGSCCGCGGC 1560  
Db 8138 AGGGCTGGGTGGCCCAACTGGGATGCCACTGGAGCCCCACCCAGGAGCTGSCCGCGGC 8197  
Qy 1561 ACCTTACGCTTCAGCTGTGTGATCCGCTGCTCCCTCTTTTGGGGTAGATGCGGCCCCGAT 1620  
Db 8198 ACCTTACGCTTCAGCTGTGTGATCCGCTGCTCCCTCTTTTGGGGTAGATGCGGCCCCGAT 8257  
Qy 1621 CAGGCTGACTGCTGCTCTTTTGTTCCTTCTGTCTGCTCGAACCACTTGCTGCTGGGC 1680  
Db 8258 CAGGCTGACTGCTGCTCTTTTGTTCCTTCTGTCTGCTCGAACCACTTGCTGCTGGGC 8317  
Qy 1681 TAATCCCTCCCTCTTCTCCACCCGCGCACTGGGGAAGTCAAGAAATGGGGCTTGGGGCTCT 1740  
Db 8318 TAATCCCTCCCTCTTCTCCACCCGCGCACTGGGGAAGTCAAGAAATGGGGCTTGGGGCTCT 8377  
Qy 1741 CAGGAGAACTGCTTCCCTTGGCAGAGCTGGGTGGCAGCTTTCCTCCACCGGACACCG 1800  
Db 8378 CAGGAGAACTGCTTCCCTTGGCAGAGCTGGGTGGCAGCTTTCCTCCACCGGACACCG 8437  
Qy 1801 ACCCGCCCGCGCTGCTGCGCTGGGAGTGTGCGCTTTCACATGACACGCGTCTCTCC 1860  
Db 8438 ACCCGCCCGCGCTGCTGCGCTGGGAGTGTGCGCTTTCACATGACACGCGTCTCTCC 8497  
Qy 1861 TTTTGGGTGCAATGCTATTTCATTTTGACGCGACAGCCAGTGTATTTAACAGTCACTA 1920  
Db 8498 TTTTGGGTGCAATGCTATTTCATTTTGACGCGACAGCCAGTGTATTTAACAGTCACTA 8557  
Qy 1921 TTGATGGACATTTGGTGTGTTTCCCATCTTTTGTACCATAAATAATAGGCATAGTAAA 1980  
Db 8558 TTGATGGACATTTGGTGTGTTTCCCATCTTTTGTACCATAAATAATAGGCATAGTAAA 8617  
Qy 1981 AAAAAAAAAAAAAA 1994  
Db 8618 AAAAAAAAAAAAAA 8631

## RESULT 11

ABD20693

ID ABD20693 standard; DNA; 8631 BP.

XX

AC ABD20693;

XX

DT 29-JUL-2004 (first entry)

XX

DE Human pulmonary and inflammatory target DNA #304.

XX

KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KW surfactant depletion; antiallergic; antiinflammatory; antispasmodic;  
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;  
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KW pulmonary transplantation rejection; ds.

OS Homo sapiens.

XX

PN WO200285309-A2.

XX



Db 7958 GGCACCTGACTTCTGTGTCCTCCCAAGTGCAGTATCAGGCCCCCTGATATGACACACCTCTGCA 8017  
Qy 1381 GATACATGTCATGAGTGCATTTAGTAGGGCCGCGCAGTGCAAGGCCACTGCTGCCCCGA 1440  
Db 8018 GATACATGTCATGAGTGCATTTAGTAGGGCCGCGCAGTGCAAGGCCACTGCTGCCCCGA 8077  
Qy 1441 GGAAGTCCCGGACCGTGCAGTCTGCGCTTTCTCTCCCGCTGCTAGCCAGGATGA 1500  
Db 8078 GGAAGTCCCGGACCGTGCAGTCTGCGCTTTCTCTCCCGCTGCTAGCCAGGATGA 8137  
Qy 1501 AGGGCTGGGTGGCCACAACATGGATGCGCACTGGAGCCGCCACCCAGGAGTGGCCCGGC 1560  
Db 8138 AGGGCTGGGTGGCCACAACATGGATGCGCACTGGAGCCGCCACCCAGGAGTGGCCCGGC 8197  
Qy 1561 ACCTTACGCTTACGCTTTCATCCGCTGCTGCTCCCTTTTGGGTAGATGCGGCCCGAT 1620  
Db 8198 ACCTTACGCTTTCAGCTTGTGATCCGCTGCTGCTCCCTTTTGGGTAGATGCGGCCCGAT 8257  
Qy 1621 CAGGCTGACTGCTGCTCTTTTGTTCCTTCTGCTCGAACCACTTGGCTCGGC 1680  
Db 8258 CAGGCTGACTGCTGCTCTTTTGTTCCTTCTGCTCGAACCACTTGGCTCGGC 8317  
Qy 1681 TAATCCTCCTTCTTCTCCACCGCACTGGGGAAGTCAAGAAATGGGCTTGGGCTCT 1740  
Db 8318 TAATCCTCCTTCTTCTCCACCGCACTGGGGAAGTCAAGAAATGGGCTTGGGCTCT 8377  
Qy 1741 CAGGGAAGTCTTCCCTGCGAGAGCTGGGTGGGAGCTCTTCTCCACCGGACCG 1800  
Db 8378 CAGGGAAGTCTTCTCCCTGCGAGAGCTGGGTGGGAGCTCTTCTCCACCGGACCG 8437  
Qy 1801 ACCCGCCGCGCTGCTGCTGGAGTGTGCTTACCATGACACCGGTGCTCTCC 1860  
Db 8438 ACCCGCCGCGCTGCTGCTGGAGTGTGCTTACCATGACACCGGTGCTCTCC 8497  
Qy 1861 TTTTGGGCTGCATGCTATTCATTTTTCAGCCAGACCGATGTATTTAAACAGTCACTA 1920  
Db 8498 TTTTGGGCTGCATGCTATTCATTTTTCAGCCAGACCGATGTATTTAAACAGTCACTA 8557  
Qy 1921 TTGATGCAATTTGGGTGTTTCCCATCTTTTGTACCAATAATAGGCATAGTAA 1980  
Db 8558 TTGATGCAATTTGGGTGTTTCCCATCTTTTGTACCAATAATAGGCATAGTAA 8617  
Qy 1981 AAAAAAAAAAAAAA 1994  
Db 8618 AAAAAAAAAAAAAA 8631  
RESULT 12  
ID ADQ87415 standard; cDNA; 1967 BP.  
AC ADQ87415;  
XX ADQ87415;  
XX ADQ87415;  
DT 07-OCT-2004 (first entry)  
TX Human tumour-associated antigenic target (TAT) cDNA sequence #4292.  
DE human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;  
XX cancer; cell proliferative disorder; gene; ss.  
XX Homo sapiens.  
XX WO2004060270-A2.  
PN 22-JUL-2004.  
XX 15-OCT-2003; 2003WO-US029126.  
XX 18-OCT-2002; 2002US-0418988P.  
PR (GETH ) GENENTECH INC.  
XX (WUTD/) WU T D.  
PA

(ZHOU/) ZHOU Y.  
Wu TD, Zhou Y;  
WPI; 2004-534300/51.  
New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.  
Claim 1; SEQ ID NO 4292; 5504pp; English.  
The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridizes to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.  
Sequence 1967 BP; 409 A; 581 C; 629 G; 348 T; 0 U; 0 Other;  
Query Match 98.0%; Score 1954.4; DB 13; Length 1967;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1966; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
Qy 9 CATGCCCTTGTGATCCAGGTGGGNAACTAGGCCCCAGAGAGTCCAGACCCCGCAGAC 68  
Db 1 CATGCCCTTGTGATCCAGGTGGGNAACTAGGCCCCAGAGAGTCCAGACCCCGCAGAC 60  
Qy 69 TATCAATCCAGTCTCTTCCCTCACTCCCTGTGAAGTCTCCAGCATCATCGAGTCCC 128  
Db 61 TATCAATCCAGTCTCTTCCCTCACTCCCTGTGAAGTCTCCAGCATCATCGAGTCCC 120  
Qy 129 ATCAGCCCTTGGCTTGTGGATGAATAGCACCTCTGGAAGAGCCCACTGTGTGAGATGG 188  
Db 121 ATCAGCCCTTGGCTTGTGGATGAATAGCACCTCTGGAAGAGCCCACTGTGTGAGATGG 180  
Qy 189 TGCAGCCAGTGGTGGCCCGGAGAGATCAGAGTACTGGGCGGAGAGTCTCCTCTGG 248  
Db 181 TGCAGCCAGTGGTGGCCCGGAGAGATCAGAGTACTGGGCGGAGAGTCTCCTCTGG 240  
Qy 249 GGAAGCCAGCATGTCTGACCTGCTTCAGAACAGGGCGCTCTCTGAGACCTCCAGCGCT 308

Db 241 GGAAGCCAGCATGCTGCACCTGCTTCAGAAACAGGGCGCTCTGAGACCTCCAGCGCT 300  
Qy 309 GCCTGGAGGAGATCAAGAGCTCGAGATGCCATCCGGCAGAGCAACAGATTCTCGCGG 368  
Db 301 GCCTGGAGGAGATCAAGAGCTCGAGATGCCATCCGGCAGAGCAACAGATTCTCGCGG 360  
Qy 369 AGCCTCGAGGAGCTTCTGCATTTCCAGCCAGCCAGAGGAGGAGAGGATTCTCTCA 428  
Db 361 AGCCTCGAGGAGCTTCTGCATTTCCAGCCAGCCAGAGGAGGAGAGGATTCTCTCA 420  
Qy 429 TGTCAAGTTCCAGGAGCCAGGAACTGCTGGAGAGACTCGGCCTGGAGAAAGCTCGATC 488  
Db 421 TGTCAAGTTCCAGGAGCCAGGAACTGCTGGAGAGACTCGGCCTGGAGAAAGCTCGATC 480  
Qy 489 TGAAGAGCAGAGGAGGAGGCTCTCGGGAGGTGAGCAGCTGAGAGATGCCAGCAGC 548  
Db 481 TGAAGAGCAGAGGAGGAGGCTCTCGGGAGGTGAGCAGCTGAGAGATGCCAGCAGC 540  
Qy 549 AGATGGCTGAGGACAAAGGCTCTGTGAAGCCAGGTGACGTCTTGTCTCGGGAGGCTGC 608  
Db 541 AGATGGCTGAGGACAAAGGCTCTGTGAAGCCAGGTGACGTCTTGTCTCGGGAGGCTGC 600  
Qy 609 AGAGAGCCAGAGTCTGCTGGAGGCTGCTCAAGGAATGCCAGGCTCTGGAGGCTCGGG 668  
Db 601 AGAGAGCCAGAGTCTGCTGGAGGCTGCTCAAGGAATGCCAGGCTCTGGAGGCTCGGG 660  
Qy 669 CCCGGGCGGACGAGAGAGGCGGCGAGCTGGAGAGTGGAGCGCAGCGCTGCAAGCAGC 728  
Db 661 CCCGGGCGGACGAGAGAGGCGGCGAGCTGGAGAGTGGAGCGCAGCGCTGCAAGCAGC 720  
Qy 729 AGCAGCGCTGAGGTGAGCCAGCTGCGCATGACAGGCGCAGAGCGTGGAGCGCGGCTCC 788  
Db 721 AGCAGCGCTGAGGTGAGCCAGCTGCGCATGACAGGCGCAGAGCGTGGAGCGCGGCTCC 780  
Qy 789 GCATGAGCGCCAGGCGGCTCGAGGAGAGAGAGAGCTGGCCAGTTGAGGTGGCGCT 848  
Db 781 GCATGAGCGCCAGGCGGCTCGAGGAGAGAGAGAGCTGGCCAGTTGAGGTGGCGCT 840  
Qy 849 ATCACCAGCTCTTCCAAAGAAATACGAAACCAATCAAGAGCAGCGTGGTGGGCGAGTGC 908  
Db 841 ATCACCAGCTCTTCCAAAGAAATACGAAACCAATCAAGAGCAGCGTGGTGGGCGAGTGC 900  
Qy 909 GGNAGCGAGATGACGCTGGAAGATCTCAACAGCAGCTCCAGCAGCGCAGGAGGCGCC 968  
Db 901 GGAAGCGAGAAATGACGCTGGAAGATCTCAACAGCAGCTCCAGCAGCGCAGGAGGCGCC 960  
Qy 969 TGTGGCCAAACAGAGGATGATCGATAAGCTGAAGGAGGAGGCGCAGCAGCAAGATTG 1028  
Db 961 TGTGGCCAAACAGAGGATGATCGATAAGCTGAAGGAGGAGGCGCAGCAGCAAGATTG 1020  
Qy 1029 TGATGAGACCGTTCCGCTGCTGAAGGCGCCAGGCGGATATCTCAAGCGGAGCTTCCAGG 1088  
Db 1021 TGATGAGACCGTTCCGCTGCTGAAGGCGCCAGGCGGATATCTCAAGCGGAGCTTCCAGG 1080  
Qy 1089 CTGAGAGCAGCCCGGAGAGAGCTGGCCGAGAGAAAGAGCTCTCTGAGAGCAGCTGG 1148  
Db 1081 CTGAGAGCAGCCCGGAGAGAGCTGGCCGAGAGAAAGAGCTCTCTGAGAGCAGCTGG 1140  
Qy 1149 AGCAGCTGAGAGGAGTACAGCAAACTGAAGGCGCAGCTGTCAGGAGTCCGCGCAGGATCG 1208  
Db 1141 AGCAGCTGAGAGGAGTACAGCAAACTGAAGGCGCAGCTGTCAGGAGTCCGCGCAGGATCG 1200  
Qy 1209 AGGACATGAGAGCGGATGTCAGAGTCTCCAGGCGCCCTTGTGCCCGCCCGCTGCTGCT 1268  
Db 1201 AGGACATGAGAGCGGATGTCAGAGTCTCCAGGCGCCCTTGTGCCCGCCCGCTGCTGCT 1260  
Qy 1269 ACCTCTCTCTCCCTGCGCTGCGCAGCAGAGAGGAGGCGCCCGCAGAGAGCGCACCTG 1328  
Db 1261 ACCTCTCTCTCTCCCTGCGCTGCGCAGCAGAGAGGAGGCGCCCGCAGAGAGCGCACCTG 1320  
Qy 1329 ACTTCTGTGTCACCAAGTGCAGATATCAGGCGCCCTGATATGAGCACCCCTCAGATACATG 1388

Db 1321 ACTTCTGTGTCACCAAGTGCAGATATCAGGCGCCCTGATATGAGCACCCCTGCAGATACATG 1380  
Qy 1389 TCATGAGTGCATTGAGTAGGGCCGGCCAGTCAAGGCCACTGCTCTGCCCGAGGAGCTGC 1448  
Db 1381 TCATGAGTGCATTGAGTAGGGCCGGCCAGTCAAGGCCACTGCTCTGCCCGAGGAGCTGC 1439  
Qy 1449 CCGGACCGTGCAGTCTGCGCTTCTCTCCCGCTGCTAGCCAGGATGAAGGCTGC 1508  
Db 1440 CCGGACCGTGCAGTCTGCGCTTCTCTCCCGCTGCTAGCCAGGATGAAGGCTGC 1499  
Qy 1509 GTGGCCCAACTGGGATGCCACCTGGAGGCGCCACCCAGGAGTGGCCCGGACCTTACG 1568  
Db 1500 GTGGCCCAACTGGGATGCCACCTGGAGGCGCCACCCAGGAGTGGCCCGGACCTTACG 1559  
Qy 1569 CTTGAGCTGTTGATCCGCTGCTGCCCTCTTTTGGGGTAGATGCGGCGCCCGATCAGGCGCTG 1628  
Db 1560 CTTGAGCTGTTGATCCGCTGCTGCCCTCTTTTGGGGTAGATGCGGCGCCCGATCAGGCGCTG 1619  
Qy 1629 ACTGCTGCTCTTTTGTGTTCCCTTCTGCTGCTCGAACCACTTGGCTCGGGCTAATCCCT 1688  
Db 1620 ACTGCTGCTCTTTTGTGTTCCCTTCTGCTGCTCGAACCACTTGGCTCGGGCTAATCCCT 1679  
Qy 1689 CCCTCTTCTCCACCCGCGCACTGGGGAAGTCAAGAAATGGGCGCTGGGCTCTCAGGGAGA 1748  
Db 1680 CCCTCTTCTCCACCCGCGCACTGGGGAAGTCAAGAAATGGGCGCTGGGCTCTCAGGGAGA 1739  
Qy 1749 ACTGCTTCCCTGGCAGAGTGGGTGGAGCTTCTTCCACCCGAGACCCGCGCGCC 1808  
Db 1740 ACTGCTTCCCTGGCAGAGTGGGTGGAGCTTCTTCCACCCGAGACCCGCGCGCC 1799  
Qy 1809 GCGCTGTGCGCTGGGAGTGTGCTGCTTACCATGCACAGGAGTGTCTCTCTTTTGGGC 1868  
Db 1800 GCTGTGTGCGCTGGGAGTGTGCTGCTTACCATGCACAGGAGTGTCTCTCTTTTGGGC 1859  
Qy 1869 TGCATGCTATTCCATTTTGCAGCCAGACCCAGTGTATTTAAACAGTCACTATTGATGGA 1928  
Db 1860 TGCATGCTATTCCATTTTGCAGCCAGACCCAGTGTATTTAAACAGTCACTATTGATGGA 1919  
Qy 1929 CATTTGGTGTGTTCCCATCTTTTGTACCATAAATAATGGCATAGT 1976  
Db 1920 CATTTGGTGTGTTCCCATCTTTTGTACCATAAATAATGGCATAGT 1967

## RESULT 13

ADQ86256

ID ADQ86256 standard; cDNA; 1967 BP.

XX ADQ86256;

AC

XX 07-OCT-2004 (first entry)

DT

XX Human tumour-associated antigenic target (TAT) cDNA sequence #3128.

DE

XX human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;

KW cancer; cell proliferative disorder; gene; ss.

XX Homo sapiens.

OS

PN WO2004060270-A2.

XX

XX 22-JUL-2004.

PD

XX 15-OCT-2003; 2003WO-US029126.

PF

XX 18-OCT-2002; 2002US-0419988P.

PR

XX (GETH) GENENTECH INC.

PA (WUTD/) WU T D.

PA (ZHOU/) ZHOU Y.

XX

PI Wu TD, Zhou Y;

XX WPI; 2004-534300/51.

DR



XX New nucleic acid molecule and encoded polypeptide, for diagnosing,  
PT preventing or treating cell proliferative disorders such as cancer.  
XX  
XX Claim 1; SEQ ID NO 3128; 5504pp; English.  
XX  
CC The present invention describes an isolated tumour-associated antigenic  
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide  
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of  
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%  
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-  
CC (c). Also described: (1) an expression vector comprising the above  
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)  
CC a process for producing a polypeptide; (4) an isolated polypeptide  
CC comprising: (a) an amino acid sequence encoded by any of the above  
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-  
CC length coding region of the above nucleotide sequences; or (c) a sequence  
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide  
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)  
CC an isolated antibody that binds to the above polypeptide; (7) a process  
CC for producing the antibody; (8) an isolated oligopeptide that binds to  
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)  
CC binding organic molecule that binds to the above polypeptide; (10) a  
CC composition of matter comprising the above (chimeric) polypeptide,  
CC antibody, oligopeptide or TAT binding organic molecule, in combination  
CC with a carrier; (11) an article of manufacture comprising a container and  
CC the composition of matter contained within the container; (12) methods of  
CC inhibiting the growth of a cell that expresses the above protein, where  
CC the growth of the cell is at least in part dependent upon a growth  
CC potentiating effect of the above protein; (13) a method of  
CC therapeutically treating a mammal having a cancerous tumour comprising  
CC cells that express the above protein; (14) a method of determining the  
CC presence of a protein in a sample suspected of containing the protein  
CC described above; (15) methods of diagnosing the presence of a tumour in a  
CC mammal; (16) a method for treating or preventing a cell proliferative  
CC disorder associated with increased expression or activity of the above  
CC protein; and (17) a method of binding an antibody, oligopeptide or  
CC organic molecule to a cell that expresses the protein described above.  
CC The TAT sequences have cytostatic activities, and can be used in gene  
CC therapy. The composition and methods are useful for diagnosing,  
CC preventing or treating cancer. The composition is also useful for preparing  
CC a medicament for the therapeutic treatment or diagnostic detection of a  
CC cell proliferative disorder or cancer. The present sequence represents a  
CC human TAT cDNA sequence from the present invention.  
XX  
SQ Sequence 1967 BP; 409 A; 581 C; 629 G; 348 T; 0 U; 0 Other;

Query Match 98.0%; Score 1954.4; DB 13; Length 1967;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1966; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 9 CATGGCCCTTGATCCAGTGGGGAACCTAAGGCCCCAGAGAAGTAGAACCCCGCAGAC 68  
DB 1 CATGGCCCTTGATCCAGTGGGGAACCTAAGGCCCCAGAGAAGTAGAACCCCGCAGAC 60  
QY 69 TATCAATCCAGTCTCTCCCTCACTCCCTGTGAAGCTCTCCAGCATCATCGAGTCCC 128  
DB 61 TATCAATCCAGTCTCTCCCTCACTCCCTGTGAAGCTCTCCAGCATCATCGAGTCCC 120  
QY 129 ATCAGCCCTTGCCCTTTGGATGAATAGGCACCTCTGGAAGGCCCACTGTGTGAGATGG 188  
DB 121 ATCAGCCCTTGCCCTTTGGATGAATAGGCACCTCTGGAAGGCCCACTGTGTGAGATGG 180  
QY 189 TGCAGCCCATGTGGTGGCCCGGACAGATCAGGACGTACTGGGCGAAGATCTCTCTCG 248  
DB 181 TGCAGCCCATGTGGTGGCCCGGACAGATCAGGACGTACTGGGCGAAGATCTCTCTCG 240  
QY 249 GGAAGCCAGCATGCTGACCTGCTTCAAGACAGGGCGCTCTGAGACCTCCACGCGCT 308  
DB 241 GGAAGCCAGCATGCTGACCTGCTTCAAGACAGGGCGCTCTGAGACCTCCACGCGCT 300  
QY 309 GCCTGGAGAGAAATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACCAAGATTTCTCGGG 368  
DB

DB 301 GCCTGGAGAGAAATCAAGAGCTCCGAGATGCCATCCGGCAGAGCAACCAAGATTTCTCGGG 360  
QY 369 AGCGCTGCCAGAGAGCTTCTGCAATTTTCCAAAGCCAGCCAGAGGGAGGAGAGGAGTTCTCTCA 428  
DB 361 AGCGCTGCCAGAGAGCTTCTGCAATTTTCCAAAGCCAGCCAGAGGGAGGAGAGGAGTTCTCTCA 420  
QY 429 TGTGCAAGTTCCAGAGAGGCCAGGAAACTGTTGGAGAGACTTCGGCCTTGGAGAACTCGATC 488  
DB 421 TGTGCAAGTTCCAGAGAGGCCAGGAAACTGTTGGAGAGACTTCGGCCTTGGAGAACTCGATC 480  
QY 489 TGAAGAGGAGAGAGAGAGAGAGCTCTGCGGGAGGTGGAGCACTTGAAGAGATGCGAGCAGC 548  
DB 481 TGAAGAGGAGAGAGAGAGAGAGCTCTGCGGGAGGTGGAGCACTTGAAGAGATGCGAGCAGC 540  
QY 549 AGATGCTCAGAGACAGAGGCTCTGTGAAGCCAGGTGAGCTGCTTGTCTCGGGAGCTGC 608  
DB 541 AGATGCTCAGAGACAGAGGCTCTGTGAAGCCAGGTGAGCTGCTTGTCTCGGGAGCTGC 600  
QY 609 AGGAGAGCCAGAGTTCGCTTGGAGGCTGCCAATAAGGAATGCCAGGCTCTGGAGGGTCTGGG 668  
DB 601 AGGAGAGCCAGAGTTCGCTTGGAGGCTGCCAATAAGGAATGCCAGGCTCTGGAGGGTCTGGG 660  
QY 669 CCGGGCGGCCAGAGAGAGAGAGGCGGCGAGCTGGAGAGTGAAGCGGCTGTCAGCAGC 728  
DB 661 CCGGGCGGCCAGAGAGAGAGAGGCGGCGAGCTGGAGAGTGAAGCGGCTGTCAGCAGC 720  
QY 729 AGCAGAGCTGAGGTGGACCACTGCGCATCCAGGGCCAGAGCGCTGGAGGGCGCGCTCC 788  
DB 721 AGCAGAGCTGAGGTGGACCACTGCGCATCCAGGGCCAGAGCGCTGGAGGGCGCGCTCC 780  
QY 789 GCATGGAGCCCGAGGCGGCTCCGAGGAGAGAGAGAGTGGCCCACTGTTGCAGGTGGCCT 848  
DB 781 GCATGGAGCCCGAGGCGGCTCCGAGGAGAGAGAGAGTGGCCCACTGTTGCAGGTGGCCT 840  
QY 849 ATCAGCAGCTTTCAGAAATACGACCAACATCAAGAGAGCGGTGGTGGCAGTGAGC 908  
DB 841 ATCAGCAGCTTTCAGAAATACGACCAACATCAAGAGAGCGGTGGTGGCAGTGAGC 900  
QY 909 GGAAGCGAGAAATCAGCTGGAGAGTCTCAACACAGCAGCTCCAGCAGGCGGAGGAGGCC 968  
DB 901 GGAAGCGAGAAATCAGCTGGAGAGTCTCAACACAGCAGCTCCAGCAGGCGGAGGAGGCC 960  
QY 969 TGGTGGCCCAACAGAGAGTGCATTAAGCTGAAGGAGAGGAGCGCCAGCAGCACAAGATTG 1028  
DB 961 TGGTGGCCCAACAGAGAGTGCATTAAGCTGAAGGAGAGGAGCGCCAGCAGCACAAGATTG 1020  
QY 1029 TGAATGAGACCTTCCGCTGCTGAAGGCCAGCGGATATCTCAAGCGGAGTTCACAGG 1088  
DB 1021 TGAATGAGACCTTCCGCTGCTGAAGGCCAGCGGATATCTCAAGCGGAGTTCACAGG 1080  
QY 1089 CTGAGAGGAGCGCCCGGAGAGCTGGCCGAGAGAGAGAGTCTCTGCGAGGAGCAGCTGG 1148  
DB 1081 CTGAGAGGAGCGCCCGGAGAGCTGGCCGAGAGAGAGAGTCTCTGCGAGGAGCAGCTGG 1140  
QY 1149 AGCAGCTGCGAGAGGAGTACAGCAAACTGAAGCCAGCTGTCAAGAGTGGCCAGGATCG 1208  
DB 1141 AGCAGCTGCGAGAGGAGTACAGCAAACTGAAGCCAGCTGTCAAGAGTGGCCAGGATCG 1200  
QY 1209 AGGACATGAGGAAGCGGATGTGCGAGGTCTCCAGGCCCCCTTGGCCCCCGCCCTGCCT 1268  
DB 1201 AGGACATGAGGAAGCGGATGTGCGAGGTCTCCAGGCCCCCTTGGCCCCCGCCCTGCCT 1260  
QY 1269 ACCTCTCTCTCCCTGGCCCTGCGCCAGCCAGAGAGAGGAGCCCCCGGAGGAGCCACCTG 1328  
DB 1261 ACCTCTCTCTCTCCCTGGCCCTGCGCCAGCCAGAGAGGAGAGCCCCCGGAGGAGCCACCTG 1320  
QY 1329 ACTTCTGCTGCTCCCAAGTGCAGATATCAGGCCCTCTGATATGGAACACCTTCAGATACATG 1388  
DB 1321 ACTTCTGCTGCTCCCAAGTGCAGATATCAGGCCCTCTGATATGGAACACCTTCAGATACATG 1380  
QY 1389 TCATGAGGTGCATTCAGTAGGGCCCGCCAGTGCAGAGGCCACTGCTTGGCCCCCGGAGGAGCTGC 1448  
DB 1381 TCATGAGGTGCATTCAGTAGGGCCCGCCAGTGCAGAGGCCACTGCTTGGCCCCCGGAGGAGCTGC 1439





Db 529 AGAGGAGAGGAGGAGGCTCTGCGGAGGTGGAGCACTGAAGAGATGCCAGACGAGA 588  
QY 552 TGGCTAGAGACAAGGCTCTGTGAAGCCAGGTGACGTCTTGTGCTCGGGAGCTGCGAG 611  
Db 589 TGGCTAGAGACAAGGCTCTGTGAAGCCAGGTGACGTCTTGTGCTCGGGAGCTGCGAG 648  
QY 612 AGAGCCAGAGTGGCTTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGGTTCGGGCC 671  
Db 649 AGAGCCAGAGTGGCTTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGGTTCGGGCC 708  
QY 672 GGGGCGCCAGCAGCAGGCGCGGCAAGCTGGAGAGTGAGCGCAGGCGCTGTCAGCAGCAGC 731  
Db 709 GGGGCGCCAGCAGCAGGCGCGGCAAGCTGGAGAGTGAGCGCAGGCGCTGTCAGCAGCAGC 768  
QY 732 ACAGCGTGCAGGTGACCAAGCTGGCATGCAAGGCGCCAGAGCGTGGAGCGCGCTCCGCA 791  
Db 769 ACAGCGTGCAGGTGACCAAGCTGGCATGCAAGGCGCCAGAGCGTGGAGCGCGCTCCGCA 828  
QY 792 TGGAGCGCCAGCGCTCGAGGAGAGAGGAAGCTGGCCAGTTGCAAGTGGCGCTATC 851  
Db 829 TGGAGCGCCAGCGCTCGAGGAGAGAGGAAGCTGGCCAGTTGCAAGTGGCGCTATC 888  
QY 852 ACCAGCTCTTCCAAGAATACGACCAACCATCAAGAGCAGCGTGGTGGGCACTGAGCGGA 911  
Db 889 ACCAGCTCTTCCAAGAATACGACCAACCATCAAGAGCAGCGTGGTGGGCACTGAGCGGA 948  
QY 912 AGCGAGGAATGAGCTGGAAGATCTCAACACAGCAGCTCCAGCAGCGCGAGGCGCTGG 971  
Db 949 AGCGAGGAATGAGCTGGAAGATCTCAACACAGCAGCTCCAGCAGCGCGAGGCGCTGG 1008  
QY 972 TGGCCAAACAGAGGTGATCGATAGCTGAAGGAGGAGGCGCAGCAGCAGCAAGATTGGA 1031  
Db 1009 TGGCCAAACAGAGGTGATCGATAGCTGAAGGAGGAGGCGCAGCAGCAGCAAGATTGGA 1068  
QY 1032 TGGAGACCGTTCGGTGTGAAGGCGCCAGGCGGATATCTACAAGCGGCACTTCCAGGCTG 1091  
Db 1069 TGGAGACCGTTCGGTGTGAAGGCGCCAGGCGGATATCTACAAGCGGCACTTCCAGGCTG 1128  
QY 1092 AGAGCAGCGCCGGAGAGAGCTGGCGGAGAAAGAGAGCTCTGCAAGAGCAGCTGGAGC 1151  
Db 1129 AGAGCAGCGCCGGAGAGAGCTGGCGGAGAAAGAGAGCTCTGCAAGAGCAGCTGGAGC 1188  
QY 1152 AGCTGCAGAGGAGTACAGCAAACTGAAGGCGCAGCTGTGAGGAGTCGGCCAGATCGAGG 1211  
Db 1189 AGCTGCAGAGGAGTACAGCAAACTGAAGGCGCAGCTGTGAGGAGTCGGCCAGATCGAGG 1248  
QY 1212 ACATGAGGAAGCGCATGTGAGGCTCTCCAGGCGCCCTTGGCCCGCCCTGCTGCTACC 1271  
Db 1249 ACATGAGGAAGCGCATGTGAGGCTCTCCAGGCGCCCTTGGCCCGCCCTGCTGCTACC 1308  
QY 1272 TCTCTCTCCCTGGCCCTGCGCAGCAGAGAGAGCGCCCGCAGGAGCCACCTGACT 1331  
Db 1309 TCTCTCTCCCTGGCCCTGCGCAGCAGAGAGAGAGCGCCCGCAGGAGCCACCTGACT 1368  
QY 1332 TCTGCTGTCCCAAGTGCCAGTATCAGGCGCTGATATGACACCTTGCAAGATACATGTCA 1391  
Db 1369 TCTGCTGTCCCAAGTGCCAGTATCAGGCGCTGATATGACACCTTGCAAGATACATGTCA 1428  
QY 1392 TGGAGTGCAATTGAGTAGGCGCGCCAGTGCAGAGGCACTGCTGCGCCGAGGAGCTGCCCG 1451  
Db 1429 TGGAGTGCAATTGAGTAGGCGCGCCAGTGCAGAGGCACTGCTGCGCGAGGAGCTGCCCG 1487  
QY 1452 GGACCGTGAGTCTGGGCTTTCTCTCCCGCTGCTGCTAGCCAGGATGAAGGGCTGGGTG 1511  
Db 1488 GGACCGTGAGTCTGGGCTTTCTCTCTCCCGCTGCTGCTAGCCAGGATGAAGGGCTGGGTG 1547  
QY 1512 GCCAAGCTGGATGCCACTGGAGCGCCACCCAGGAGTGGCGCGGACCTTACGCTT 1571  
Db 1548 GCCAAGCTGGATGCCACTGGAGCGCCACCCAGGAGTGGCGCGGACCTTACGCTT 1607  
QY 1572 CAGCTGTTGATCGGTGGTCCCTCTTTTGGGGTAGATGCGGCGCCCGATCAGGCGCTGACT 1631

Db 1608 CAGCTGTTGATCGGTGGTCCCTCTTTTGGGGTAGATGCGGCCCGGATCAGGCGCTGACT 1667  
QY 1632 CGCTGCTCTTTTGTGTTCCCTTCTGCTGCTCGAACCACTTGGCTCGGGCTAATCCCTCCC 1691  
Db 1668 CGCTGCTCTTTTGTGTTCCCTTCTGCTGCTCGAACCACTTGGCTCGGGCTAATCCCTCCC 1727  
QY 1692 TCTTCTCTCACCCGCACTGGGGAGTCAAGAAATGGGGCTTGGGGCTCTCAGGGAGAACT 1751  
Db 1728 TCTTCTCTCACCCGCACTGGGGAGTCAAGAAATGGGGCTTGGGGCTCTCAGGGAGAACT 1787  
QY 1752 GCTTCCCTGCGAGAGCTGGGGTGGAGCTCTTCTCCCAACCGACACCGACCCGCGCC 1811  
Db 1788 GCTTCCCTGCGAGAGCTGGGGTGGAGCTCTTCTCCCAACCGACACCGACCCGCGCT 1847  
QY 1812 GCTGTGCGCTGGGAGTGGCTTACCATGACACGGGTGCTCTCTTTTGGGCTGC 1871  
Db 1848 GCTGTGCGCTGGGAGTGGCTTACCATGACACGGGTGCTCTCTTTTGGGCTGC 1907  
QY 1872 ATGCTATTCCATTTTGCAGCAGACCGATGTGATTTAAACCACTCACTATTGATGACAT 1931  
Db 1908 ATGCTATTCCATTTTGCAGCAGACCGATGTGATTTAAACCACTCACTATTGATGACAT 1967  
QY 1932 TTGGGTGTTTCCCATCTTTTGTATCAATAAATATGGCATAGTAAAAA 1981  
Db 1968 TTGGGTGTTTCCCATCTTTTGTATCAATAAATATGGCATAGTAAAAA 2017

## RESULT 15

ID ADA44712 standard; DNA; 1975 BP.  
XX ADA44712;  
AC ADA44712;  
XX 20-NOV-2003 (first entry)  
DT Human inhibitor-kappa B kinase-gamma encoding DNA #SEQ ID 10.  
DE Antisense oligonucleotide; cytostatic; immunosuppressive;  
KW antiinflammatory; gene therapy; hyperproliferative disorder; cancer;  
KW autoimmune; inflammatory disorder; inhibitor-kappa B kinase-gamma; gene;  
KW ds.  
XX Homo sapiens.  
OS WO2003031576-A2.  
PN 17-APR-2003.  
PD 03-OCT-2002; 2002WO-US031809.  
PF 06-OCT-2001; 2001US-00972607.  
PR (ISIS-) ISIS PHARM INC.  
PA Monia BP, Wyatt JR;  
PI WPI; 2003-457242/43.  
DR New compound having sequence targeted to nucleic acid encoding inhibitor-kappa B kinase-gamma, useful for preparing composition for treating e.g., cancer, or inflammatory or autoimmune disorder.  
PS Example 15; Page 86-88; 106pp; English.  
XX The invention relates to an antisense compound that is targeted to a nucleic acid encoding inhibitor-kappa B kinase-gamma, specifically hybridizing to the nucleic acid encoding inhibitor-kappa B kinase-gamma and inhibiting its expression. Compounds of the invention are antisense oligonucleotides comprising at least one modified internucleoside linkage, which is a phosphorothioate linkage, at least one modified sugar moiety, which is a 2'-O-methoxyethyl sugar moiety, or at least one modified nucleobase, which is a 5-methylcytosine. Preferably, the antisense oligonucleotide is a chimeric oligonucleotide. The compound of

CC the invention is useful for preparing a composition for treating a  
 CC hyperproliferative disorder e.g., cancer, or an autoimmune or  
 CC inflammatory disorder. The methods are useful for inhibiting the  
 CC expression of inhibitor-kappa B kinase-gamma in cells or tissues, and  
 CC treating an animal having a disease or condition associated with  
 CC inhibitor-kappa B kinase-gamma. The current sequence represents the human  
 CC inhibitor-kappa B kinase-gamma encoding sequence that was used to design  
 CC the antisense oligonucleotides of the invention.  
 XX  
 SQ

Sequence 1975 BP; 424 A; 576 C; 628 G; 347 T; 0 U; 0 Other;

Query Match	91.9%	Score 1832.6;	DB 8;	Length 1975;
Best Local Similarity	99.7%	Pred. No. 0;		
Matches 1846;	Conservative 0;	Mismatches 4;	Indels 1;	Gaps 1;
QY	131	CAGCCCTTGGCCCTGTTGGATGAATAGGACCTCTGGAAGAGCAACTGTGTGAGATGGTG	190	
DB	93	CAGCCCTTGGCCCTGTTGGATGAATAGGACCTCTGGAAGAGCAACTGTGTGAGATGGTG	152	
QY	191	CAGCCCAAGTGGTGGCCCGGAGAGATCAGGAGCTACTGGGGCAAGAGTCTCTCTGGGG	250	
DB	153	CAGCCCAAGTGGTGGCCCGGAGAGATCAGGAGCTACTGGGGCAAGAGTCTCTCTGGGG	212	
QY	251	AAGCAGCCATGTGCACTTGTCTTCCAGAACAGGGCGCTCTCTGAGACCTCTCAGCGCTGC	310	
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QY	311	CTGGAGGAGATCAAGAGCTCCGAGTCCAGATGCCATCCGGGAGAGCAACAGATTCGGGGAG	370	
DB	273	CTGGAGGAGATCAAGAGCTCCGAGTCCAGATGCCATCCGGGAGAGCAACAGATTCGGGGAG	332	
QY	371	CGCTGGAGGAGCTTCTGCAATTTCCAGACCCAGAGAGGAGGAGAGGAGTCTCTCATG	430	
DB	333	CGCTGGAGGAGCTTCTGCAATTTCCAGACCCAGAGAGGAGGAGAGGAGTCTCTCATG	392	
QY	431	TGCAAGTTCCAGAGGCCAGGAAAATGTFGGAGAGACTCGGCCTTGAGAACTCGATCTG	490	
DB	393	TGCAAGTTCCAGAGGCCAGGAAAATGTFGGAGAGACTCGGCCTTGAGAACTCGATCTG	452	
QY	491	AGAGGACAGAGAGAGAGAGCTCTGGGAGGAGTGGAGCACTGAAGAGATGCCAGCAGAG	550	
DB	453	AGAGGACAGAGAGAGAGAGCTCTGGGAGGAGTGGAGCACTGAAGAGATGCCAGCAGAG	512	
QY	551	ATGGCTGAGGAACAAGCCCTCTGTGAAAGCCAGAGTGAAGTCTCTTCTCGGGAGCTCGAG	610	
DB	513	ATGGCTGAGGAACAAGCCCTCTGTGAAAGCCAGAGTGAAGTCTCTTCTCGGGAGCTCGAG	572	
QY	611	GAGAGCCAGAGTCGCTTGGAGGCTGCCACTAAGAAATGCCAGAGCTCTGGAGGGTGGGGCC	670	
DB	573	GAGAGCCAGAGTCGCTTGGAGGCTGCCACTAAGAAATGCCAGAGCTCTGGAGGGTGGGGCC	632	
QY	671	CGGGGGCCGAGGAGAGCGCGGAGCTGGAGAGTGAAGAGAGGAGGAGGAGGAGGAGGAG	730	
DB	633	CGGGGGCCGAGGAGAGCGCGGAGCTGGAGAGTGAAGAGAGGAGGAGGAGGAGGAGGAG	692	
QY	731	CACAGCGTGCAGGTGGAACAAGTCCGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG	790	
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DB	813	CACAGCTCTTCCAGAGATACGACCAACACATCAAGAGAGAGGAGGAGGAGGAGGAGGAG	872	
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QY	1931	TTTGGGTTGTTTCCCATCTTTTGTACATATAAATAATGGGCTAGTAAAAA	1981	
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GenCore version 5.1.6  
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2856.666 Million cell updates/sec

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Perfect score: 2115

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	2115	100.0	2009	4	US-09-646-403-1
2	2115	100.0	2035	4	US-09-863-049B-3
3	2028.5	95.9	2034	4	US-09-646-403-2
4	1822.5	86.2	1874	4	US-09-253-701-2
5	584.5	27.6	23106	4	US-09-863-049B-1
6	251	11.9	5883	4	US-09-949-016-5001
7	237	11.2	2812	4	US-09-702-953B-1
8	237	11.2	6644	4	US-08-875-435B-5
9	236	11.2	2934	4	US-09-010-147B-17
10	235	11.1	6175	4	US-08-875-435B-1
11	228.5	10.8	3536	4	US-09-949-016-1083
12	228.5	10.8	7218	4	US-09-949-016-1775

13	228.5	10.8	7218	4	US-09-949-016-1776	Sequence 1776, Ap
14	228.5	10.8	82125	4	US-09-949-016-13517	Sequence 13517, A
15	228.5	10.8	82125	4	US-09-949-016-13518	Sequence 13518, A
16	225	10.6	5185	4	US-09-976-594-640	Sequence 640, App
17	223.5	10.6	7596	4	US-09-023-655-1463	Sequence 1463, Ap
c 18	223	10.5	945	4	US-09-543-681A-2325	Sequence 2325, Ap
19	223	10.5	3543	4	US-09-543-681A-2264	Sequence 2264, Ap
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24	222.5	10.5	6306	2	PCT-US93-06160-3	Sequence 3, Appli
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27	221	10.4	4860	4	US-09-949-016-296	Sequence 296, App
28	221	10.4	7453	4	US-09-620-312D-248	Sequence 248, App
29	221	10.4	7501	4	US-09-620-312D-249	Sequence 249, App
30	221	10.4	8948	3	US-09-643-597-119	Sequence 119, App
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33	221	10.4	8948	4	US-09-606-421B-119	Sequence 119, App
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41	217.5	10.3	3893	4	US-09-949-016-908	Sequence 908, App
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43	214.5	10.1	6861	4	US-09-949-016-1240	Sequence 1240, Ap
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#### ALIGNMENTS

##### RESULT 1

US-09-646-403-1  
; Sequence 1, Application US/09646403  
; Patent No. 6734174  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: KOVALENKO, Andrei  
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR FI  
; TITLE OF INVENTION: AND OTHER PROTEINS  
; FILE REFERENCE: WALLACH=27  
; CURRENT APPLICATION NUMBER: US/09/646,403  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: IL 123758  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: PCT/IL99/00158  
; PRIOR FILING DATE: 1999-03-18  
; PRIOR APPLICATION NUMBER: IL 126024  
; PRIOR FILING DATE: 1998-09-01  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2009  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-646-403-1

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Score: 2115.00 Matches: 419  
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Query Match: 100.00% Indels: 0  
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DB 574 TCTGTGAAAGCCAGGTGACGTCTTGTCTCGGGAGCTGCGAGGAGCCAGAGTCGCTTG 633  
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QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220  
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RESULT 2  
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; Sequence 3, Application US/09863049B  
; Patent No. 6824972  
; GENERAL INFORMATION:  
; APPLICANT: Kenrick, Sue J.  
; APPLICANT: Nelson, David L.  
; APPLICANT: Aradhya, Swaroop  
; APPLICANT: D'Urso, Michele  
; APPLICANT: Woffendin, Hayley  
; APPLICANT: Munnich, Arnold  
; APPLICANT: Smahi, Asmae  
; APPLICANT: Israel, Alain  
; APPLICANT: Poustka, Annemarie  
; APPLICANT: Lewis, Richard A  
; APPLICANT: Levy, Moise  
; APPLICANT: Heiss, Nina  
; TITLE OF INVENTION: Diagnosis and Treatment of Medical Conditions Associated with Defe  
; FILE REFERENCE: HO-P01961US1  
; CURRENT APPLICATION NUMBER: US/09/863,049B  
; CURRENT FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/206,223  
; PRIOR FILING DATE: 2000-05-22  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn version 3.1  
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; LENGTH: 2035  
; TYPE: DNA  
; ORGANISM: Human  
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Db 1206 AGCAAACTGAAGCCAGCTGTCAAGAGTCCGCCAGGATCGAGGACATGAGGAAGCGCAT 1265
QY 361 ValGluValSerGlnAlaProLeuProProAlaProAlaTyrLeuSerSerProLeuAla 380
Db 1266 GTCGAGCTCTCCAGGCCCCCTTGGCCCCCGCCCTGCCCTACCTCTCTCCCTCGGCC 1325
QY 381 LeuProSerGlnArgArgSerProProGluProProAlaPheCysCysProLysCys 400
Db 1326 CTGCCAGCCAGAGGAGGAGCCCCCGAGAGCCACCTGACTTCTGCTGTGCCAAGTGC 1385
QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
Db 1386 CAGTATCAGGCCCTGTATGGACACCTGCAGATACATGTCTATGGAGTGCATTGAG 1442
```

## RESULT 3

```
US-09-646-403-2
; Sequence 2, Application US/09646403
; Patent No. 6734174
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: KOVALENKO, Andrei
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR
; TITLE OF INVENTION: AND OTHER PROTEINS
```

```
; FILE REFERENCE: WALLACH=27
; CURRENT APPLICATION NUMBER: US/09/646, 403
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: IL 123758
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: PCT/IL99/00158
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: IL 126024
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 2034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-646-403-2

Alignment Scores:
Pred. No.: 7e-192 Length: 2034
Score: 2028.50 Matches: 413
Percent Similarity: 97.64% Conservative: 0
Best Local Similarity: 97.64% Mismatches: 6
Query Match: 95.91% Indels: 4
DB: 4 Gaps: 1

US-09-377-795-2 (1-419) x US-09-646-403-2 (1-2034)
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QY 1 MetAsnArgHisLeuThrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
Db 172 ATGAATAGGCACCTCTGGAAGAGACCAACTGTGTGAGATGTTGAGATGTTGAGTGGCCG 231
QY 21 AlaAlaAspGlnAspValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40
Db 232 GCAGCAGATCAGGACGCTACTTGGCGGAAGAGTCTCTCTGGGGAAGCCAGCATGCTGCAC 291
QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeu-GluGluHisGlnG 60
Db 292 CTGCTCTCAAGAACAGGCGCTCTGAGACCTCTCCAGCGCTGCTGGGAGGAGAATCAAGA 351
QY 60 uLeuArgAspAlaIleArgGln-SerAsnGlnIleLeuArgGluArgCysGlu---GluL 79
Db 352 GCTCCAGATGCCATCCGCGAGTAGCAACAGATTCTTTCGGGAGCTGCCGGAAGGAGCT 411
QY 79 euLeuHis-PheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGln 98
Db 412 TTTCTGATTTTCCAGCCAGCCAGAGGAGGAGAGAGTTCCTCTCATGTCTCAAGATTTCCAG 471
QY 99 GluAlaArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLys 118
Db 472 GAGGCCAGGAAACTGTGTGGAGAGACTCGGCTTCGAGAGCTCGATCTGAAGAGGAGAGAG 531
QY 119 GluGlnAlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAsp 138
Db 532 GAGCAGGCTCTGCGGAGGTGGAGCACCTGAAGAGATGCCAGGCTCTGGAGGGTCCGGCCG 591
QY 139 LysAlaSerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSer 158
Db 592 AAGGCTCTGTGAACCCAGGTTGAGCTCTTGTCTCGGGAGCTGCAGGAGAGCCAGAGT 651
QY 159 ArgLeuGluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSer 178
Db 652 CGCTTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGGTCCGGCCCGGGCCGAGC 711
QY 179 GluGlnAlaArgGlnLeuGlnSerGluArgGluAlaLeuGlnGlnGlnHisSerValGln 198
Db 712 GAGCAGCGCGGAGCTGGAGAGTGAAGCGAGCGCTGCAGCAGCAGCAGCAGCAGCTGCAG 771
QY 199 ValAspGlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGln 218
Db 772 GTGACACAGCTGCGCATGAGGCCAGAGCGTGGAGGCCGCTCGCATGAGAGCCGAGCAG 831
QY 219 AlaAlaSerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPhe 238
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Db 832 GCCCCTCGGAGGAGAGAGAGCTGGCCCGAGCTTGCAGGTGGCTTATCACAGCTCTTC 891  
Qy 239 GlnGluTyrAspAenHisIleLysSerValValGlySerGluArgLysArgGlyMet 258  
Db 892 CAAGAATACGACACACATCAAGAGCAGCGTGGTGGCAGTGAGCGGAAGCGAGGAATG 951  
Qy 259 GlnLeuGluAspLeuLysGlnGlnLeuGlnAlaGluGluAlaLeuValAlaLysGln 278  
Db 952 CAGTGTGAAGATCTCAACAGCAGCTCCAGCAGCGCCGAGGAGCCCTGGTGCCAAACAG 1011  
Qy 279 GluValIleAspLysLeuLysGluAlaGluGlnHisLysIleValMetGluThrVal 298  
Db 1012 GAGGTGATCGATAAGCTGAAGGAGGAGGCCAGCAGCACAAGATTGTGATGAGACCGTT 1071  
Qy 299 ProValLeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAla 318  
Db 1072 CCGGTGTCGAAGCCCAAGCGGATATCTCAAGCGGACTTCCAGGCTGAGAGGCGAGGCC 1131  
Qy 319 ArgGluLysLeuAlaGluLysLysGluLeuLeuGlnGlnGlnLeuGlnGlnArg 338  
Db 1132 CGGAGAGCTGGCCGAGAGAGAGAGCTCTCGCAGAGCAGCTGAGCAGCTGAGAGG 1191  
Qy 339 GluTyrSerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLys 358  
Db 1192 GAGTACAGCAAACTGAAGGCCAGCTGTCAAGGAGTGGCCAGGATCGAGGACATGAGGAAG 1251  
Qy 359 ArgHisValGluValSerGlnAlaProLeuProLeuProAlaProAlaTyrIleuSerSerPro 378  
Db 1252 CGGATGTGAGGTCTCCAGGCCCCCTTGGCCCCCGCCCTGCTCTCTCTCTCC 1311  
Qy 379 LeuAlaLeuProSerGlnArgArgSerProProGluGluProProAspPheCysCysPro 398  
Db 1312 CTGGCCCTGCCAGCAGAGGAGGAGGCCCCCGAGGAGCCACCTGACTTCTGTCTGCC 1371  
Qy 399 LysCysGlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIle 418  
Db 1372 AAGTGCAGTATCAGGCCCTGATATGGACACCCCTGCAGATACATGTCTATGAGTGCATT 1431  
Qy 419 Glu 419  
Db 1432 GAG 1434

## RESULT 4

US-09-253-701-2  
; Sequence 2, Application US/09253701  
; Patent No. 6680366  
; GENERAL INFORMATION:  
; APPLICANT: SHOJI, YAMAKA  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCE ENCODING A MODULATOR OF NF-KB  
; FILE REFERENCE: 0660-0146-55  
; CURRENT APPLICATION NUMBER: US/09/253,701  
; CURRENT FILING DATE: 1999-02-22  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 1874  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-253-701-2

## Alignment Scores:

Pred. No.:	1,91e-171	Length:	1874
Score:	1822.50	Matches:	362
Percent Similarity:	90.93%	Conservative:	19
Best Local Similarity:	86.40%	Mismatches:	31
Query Match:	86.17%	Indels:	7
DB:	4	Gaps:	1

US-09-377-795-2 (1-419) x US-09-253-701-2 (1-1874)

Qy 1 MetAsnArgHisLeuTriLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
Db 94 ATGAACAGCACCCCTGGAGAGAACAGCTGAGTGAGAGCGGTGCAGCCCGAGTGTGGCCCA 153

Qy 21 AlaAlaAspGlnAspValLeuGluSerProLeuGlyLysProAlaMetLeuHis 40  
Db 154 GCAGAGGACCAAGCATCTGGTGAAGAACTCTTCTGGGGAAGCCTGCAATGCTACAT 213  
Qy 41 LeuProSerGluGlnGlnAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60  
Db 214 CTGCCTTTCAGAGCAGGCTACTCTTCCAGCCCTCCAGCGCTGCTGGAAGAGAATCAAGAG 273  
Qy 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80  
Db 274 CTCGAGAGCGTATCCGACAGACATCATGCTGAGGGAACGCTGTGAGAGCTGCTG 333  
Qy 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100  
Db 334 CATTTCCAGGTCCAGCGGAGGAGAGGAGTTCCTTATGTGCAAAATTCAGGAAGCC 393  
Qy 101 ArgLysLeuValGluArgLeuGluLysLeuAspLeuLeuArgGlnLysGluGln 120  
Db 394 CGGAAGCTGGTGGAGAGACTGAGCTTGGAGAGCTTGTCTCGAGTCCAGAGGAACAG 453  
Qy 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140  
Db 454 GCCTTAAAGAGTGGAGCAACTGNAAGAAATGCCAAGCAGAGATGCTGAGGACAGGCC 513  
Qy 141 SerValLysAlaGlnValThrSerLeuLeuGluGlnGlnSerGlnSerArgLeu 160  
Db 514 TCTGTAAAGCTCAGGTGACATCATTTGCTCGAGAACTCCAGGAGAGCCAGAGCCGTTG 573  
Qy 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180  
Db 574 GAGCTGCCCAAGGATCGCAAGCTTTAGAGGAGAGATTCGAGCGAGTAGTAGTCAGCAG 633  
Qy 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200  
Db 634 GTCAGACAGCTGGAGAGTGGCGGAGGTGCTACAGCAGCAGCAGCAGCGTCCAGGTGGAC 693  
Qy 201 GlnLeuArgMetGlnGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220  
Db 694 CAGCTGCTATGCAGAACCCAGAGCGTGGAGCTGCTCTTGGAAATGGAGCGGAGCTGCT 753  
Qy 221 SerGluLysArgLysLeuAlaGlnLeuValAlaTyrHisGlnLeuPheGlnGlu 240  
Db 754 TCAGAGGAGAGCGGAAGCTGGCTCAGTTCGAGCGAGCCTATCACCAACTCTTCCAGAC 813  
Qy 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260  
Db 814 TACGACAGCCACATTAAGAGCAGC-----AAGGGCATGCAGCTG 852  
Qy 261 GluAspLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280  
Db 853 GAAGATCTGAGGCACACAGCTCCAGAGCTGAGAGGCCCTGGTAGCCAAACAGGAATTG 912  
Qy 281 IleAspLysLeuLysGluAlaGluGlnHisLysIleValMetGluThrValProVal 300  
Db 913 ATTGATAAGCTGAAGAGGAGGCTGAGCAGCACAAGATTGTGATGGAGACTGTGCCAGTC 972  
Qy 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320  
Db 973 TTGAAGGCCCGAGCGGATATCTCAAGGCTGACTTCAAGCTGAGAGGCGATGCCCGGAG 1032  
Qy 321 LysLeuAlaGluLysLysGluLeuLeuGlnGlnGlnLeuGlnLeuArgGluTyr 340  
Db 1033 AAGCTGTGAGAGAGAGGAGTATTTGCAGAGCAGCTGAGCAGCTGAGCGCGAGTTC 1092  
Qy 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysArgHis 360  
Db 1093 AACAAAGCTGAAGTGGCTGCCATGAGTCAGCAGGATTCAGGATATGAGGAAGCGCAT 1152  
Qy 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380  
Db 1153 GTAGAGACTCCCGAGCGCTCTTTACTCCCTGCTCCAGCTCACCACTCTTTTCATTGTC 1212



Qy	381	LeuProSerGlnArgArgSerProProGluGluProProAspPheCysCysProLysCys	400
		***	
Db	1213	TTGTCCCAACACGGAGGAGCCCTCTCGAAGAACCTCTGACTTCTGTCGGAAGTGC	1272
Qy	401	GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu	419
Db	1273	CAGTATCAGCTCTCTGATATGGACACTCTACAGATACATGTCATGAGTGCATAGAG	1329

## RESULT 5

US-09-863-049B-1  
; Sequence 1, Application US/09863049B  
; Patent No. 6824972  
; GENERAL INFORMATION:  
; APPLICANT: Kenwick, Sue J.  
; APPLICANT: Nelson, David L.  
; APPLICANT: Aradhya, Swaroop  
; APPLICANT: D'Urso, Michele  
; APPLICANT: Woffendin, Hayley  
; APPLICANT: Munnich, Arnold  
; APPLICANT: Smahi, Asmae  
; APPLICANT: Israel, Alain  
; APPLICANT: Poustka, Annemarie  
; APPLICANT: Lewis, Richard A  
; APPLICANT: Levy, Moise  
; APPLICANT: Heiss, Nina  
; TITLE OF INVENTION: Diagnosis and Treatment of Medical Conditions Associated with Def  
; FILE REFERENCE: HO-P01961US1  
; CURRENT APPLICATION NUMBER: US/09/863,049B  
; CURRENT FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/206,223  
; PRIOR FILING DATE: 2000-05-22  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 23106  
; TYPE: DNA  
; ORGANISM: Human  
US-09-863-049B-1

Alignment Scores:			
Pred. No.:	1.06e-46	Length:	23106
Score:	584.50	Matches:	246
Percent Similarity:	18.18%	Conservative:	0
Best Local Similarity:	18.18%	Mismatches:	1
Query Match:	27.64%	Indels:	1107
DB:	4	Gaps:	5
US-09-377-795-2 (1-419) x US-09-863-049B-1 (1-23106)			
QY	173	ArgAlaArgAlaAalaSerGluGlnAlaArgGlnLeuGluSerGluArgGluAlaLeuGln	192
Db	18141	AGGGCCGGCGGCCAGCAGCAGCGCGGCGAGCTGGAGAGTGAGCGCGGCGCTGCAG	18200
QY	193	GlnGlnHisSerValGlnValaspGlnLeuArgMetGlnGlnSerValGluAlaAla	212
Db	18201	CAGCAGCAGCGTGCAGGTGCAGCAGCTGCCCATGCAGGGGCCAGCGTGGAGGCCGCG	18260
QY	213	LeuArgMetGluArgGlnAlaAalaSerGluGluLys	224
Db	18261	CTCCGCGATGCAGCGCCAGCGCGCCTCGAGGAGAGTGAGTCAGCGGGGGCGGGCGCA	18320
QY	224	-----	224
Db	18321	CCGAGGGTCTGTGGTTCTTACATTGATCTTAGCCGAAAGGCTGAGAAGTCTCGGGTCCA	18380
QY	224	-----	224
Db	18381	TGGTTCCTTCTGCCCTCTGAGGACTCCTTCAGATTCTGCCTGTGCTGTGGGCCCATTCT	18440
QY	224	-----	224
Db	18441	GTCCCTTAGCCTTGTCTAACGGTAGAGGGGACCATGATGACACCGGTTTGTCTTTGTATAC	18500

Qy	224	-----	224
Db	18501	AGTCATGCCATCTGCTCTCCAGACCACGTTTCACTCGGTGTCCACACGTCGCCTTTTTTG	18560
Qy	224	-----	224
Db	18561	TAGTTTTTTTTTCTTAGCCACTAGGTTCATCAGGGACTTGTCTTTAAACCCCTTCTAG	18620
Qy	224	-----	224
Db	18621	GCCAGTGCTGTGGCTCAGCGCTGTAAATCCCAACACTTTGGAGGCCAAGTGGGTAGAT	18680
Qy	224	-----	224
Db	18681	GGCTTAAGCCGGAGTTCCAAGACCGCTGGGCACAGAAGAACAACAAAATAFCCCC	18740
Qy	224	-----	224
Db	18741	CMAACCCCCCGTCTACCAGCATCCAATCTGGGACCTCAGGTTCCGTCTTGGCGTGCC	18800
Qy	224	-----	224
Db	18801	TTTTTCAGTCTCCTTAAATCTAGAACAGTTCCCTGCCCTTCTGAGCTGTTTGTGAAGTTC	18860
Qy	224	-----	224
Db	18861	ACAGTTTGAAGTCCAGGGTAGTTCCATTGTATTATTACTATTATTTTCAAGACAGGG	18920
Qy	224	-----	224
Db	18921	TCTVTGCTCTACCGTCCAGSCTGGAGTGGAGTGAGTGCCATAATCTCGGCTTACTGTACCTTCG	18980
Qy	224	-----	224
Db	18981	CCTCTTGTCTCAAGGATCTCCAGAGTAGCTGGGACTATAGGGCAGGCCAGCACACC	19040
Qy	224	-----	224
Db	19041	TGGCTAAATTTTTCATTTTGGTAGAGGTGGCGTTTTCTATGTTCGCCGGCTGGTCTT	19100
Qy	224	-----	224
Db	19101	GAACTCTGAGCTCAAGGATCTCTCGCTTGGCTTCTCAAAGTGTGGGATTATGGGC	19160
Qy	224	-----	224
Db	19161	GTGAGCCACCGGTCTGCGCGGATTTTATTATAAACATTAAAAATACTAGCTTTTAGGA	19220
Qy	224	-----	224
Db	19221	AAACGATATTAACTGCTGGTGACAGCCCACCAAGCCTGCTTTAGAGTTGACGGCCTC	19280
Qy	224	-----	224
Db	19281	AGGAGTCTCACACAGCCTTGAAGACCCCATTCAGSCCTGTGTGCGAGGGAGGGNAG	19340
Qy	224	-----	224
Db	19341	GAAGGGGTAGAGTTTGAAGCAGGCAGCACCGTGGCTGGACTGGGCATGAGGTGGTTTCTC	19400
Qy	225	-----ArglyseLeualaGlnleuGlnValAlaIleHisGln	236
Db	19401	CAGCAAAAGCTCCCTTTCCTCAGGAGGAAGCTGGCCCAAGTTCGAGGTGGCCTATCACAG	19460
Qy	237	LeupheGlnGlutyrAspAsnHisiIeLyseSerValValGlyserGluArgIleArg	256
Db	19461	CTCTTCCAGRATACGACAAACCATCAAGAGCAGCGTGGTGGCAGGTGACGCGAAGCGA	19520
Qy	256	-----	256
Db	19521	GTGAGTGGCACCATTGGGGCTCTTAGGGCTGGCCTTGGCTCTCTCTCTCCCGCTGGCCCT	19580





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Db 3363 GTCTGACGCTGCTCCAGGATAAAGCTGAGAGACGAAACGGGACCTTTGGGGAGAGACT 3422
Qy 333 uGluGlnLeu-
Db 3423 AGAGGCGCTGAAACACAGAGTTGGAGACACGCTGGATTCCACAGCTGCCACGAGGAGCT 3482
Qy 337 -----GlnArgGluTyrSerLysLeuLysAlaSerCysGlnGlnSerAlaAr 352
Db 3483 CAGGTCAAAACGTCAGCAGAGGTGAACATCTCTGAAGAAGACCCCTGGAGAGAGGCCAA 3542
Qy 352 g-----IleGluAspMetArgLysArgHisValGluValSerGlnAla 366
Db 3543 GACCCACGAGGCCCATCAGAGATCAGGACAGAGCAC-----TCACAGGCC 3591

RESULT 7
US-09-702-953B-1
; Sequence 1, Application US/09702953B
; Patent No. 6673897
; GENERAL INFORMATION:
; APPLICANT: VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOL
; TITLE OF INVENTION: NOVEL INHIBITORS OF NF-kappaB ACTIVATION
; FILE REFERENCE: 2676-4554US
; CURRENT APPLICATION NUMBER: US/09/702,953B
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: PCT/BE99/00055
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: 98201472.2
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2812
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (117)..(2060)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (81)..(116)
; OTHER INFORMATION:
US-09-702-953B-1

Alignment Scores:
Pred. No.: 1,74e-13 Length: 2812
Score: 237.00 Matches: 120
Percent Similarity: 39.61% Conservative: 82
Best Local Similarity: 23.53% Mismatches: 165
Query Match: 11.21% Indels: 144
DB: 4 Gaps: 20

US-09-377-795-2 (1-419) x US-09-702-953B-1 (1-2812)
Qy 16 ProSerGlyProAlaAlaAspGlnAspValLeuGlyGluGlu-----SerPro 32
Db 501 CCCTGCAATGGCGCTCTCTCGACTTGAAGTGGTCCCTACTAGGAGCAGAAATTCACCC 560
Qy 33 -----LeuGlyLysPro----- 36
Db 561 GAAACTGGGCGCCACCTACGAACATGATGGACCTGGGGGCCCCACCCACCCAGAGACAGC 620
Qy 37 ---AlaMetLeuHisLeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeu 55
Db 621 AACCTGAAGCTCCACCTG-----CAGCGCTGGAGACACCCCTTAGCGTGTGTGCA 671
Qy 56 GluGluAsn----- 59
Db 672 GAGAGCCACAGACACAGCCAGCTCTTCAACCCACCTGGGCGCGCATGGCCCTCGAGTTCAAC 731
Qy 60 GluLeuArgAspAlaIleArgGlnSerAsnGln-----IleLeuArgGluArgCys 76
Db 732 AGTTGGCCCTCAAAAGTGATAAATAATGAGCAGCGCACCTCCATCCTCGACACCTTATGT 791

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Qy 77 GluGluLeuLeuHisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLys 96
Db 792 GAGCAGCTG-----CGCCAGGAGAAATGAAGCCCTGAAGGCCAAG 830
Qy 97 PheGlnGluAlaArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLys--- 115
Db 831 CTGGCAAG-----GGCCTGGAAACAGCGGATCTGGCTGCT 866
Qy 116 -----ArgGlnLysGluGlnAlaLeuArgGluValGluHisLeuLysArgCysGln 132
Db 867 GAGAGGCTCGCGGAGAAAACACGAGCTCAAGAACTGTTGATGAACACGACAGCTCAAA 926
Qy 133 GlnGlnMetAlaGluAspLysAlaSerValLysAlaGlnValThrSerLeuLeuGlyGlu 152
Db 927 GAGGAGCTCTGTGGGCGACCCAGCTCCCAAAAGCAGAGGGTGTCTGGCAAGAGGCGTG 986
Qy 153 LeuGlnGluSerGlnSerArgLeu-----Glu 161
Db 997 GCTGACACGACGAGCGCCAGCTGTGATGGCGAGTAAAGTCCCTGAAGCGGGGCTTTTGA 1046
Qy 162 AlaAlaThrLysGluCysGlnAlaLeuGlyArgAlaArgAlaAlaSerGluGlnAla 181
Db 1047 GCAGCTGAGAAAGAAAGTGAAGTTGTAGAACACGACCAACGATGAGCTGCTGAAGTGAAC 1106
Qy 182 ArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnHisSerValGlnValAspGln 201
Db 1107 AAGCAGTGGGACCCAGCATTTCCGGTCCATGAAGCAGCAGTATGAGCAGAAATACAGAG 1166
Qy 202 LeuArg-----MetGlnGlyGlnSerValGlu---AlaAlaLeuArgMet 215
Db 1167 CTTGCCAGAAAGCTGGTGACCTGCAGAAACAGGTAACTGAGCTGGAGGCCCAACGGGAG 1226
Qy 216 GluArgGlnAlaAlaSerGluGluLysLeuAlaGlnLeuGlnValAlaTyrHis 235
Db 1227 CAGAAGCAGCGTGACTTTTGACCGGAAACTCTCTCTGGCCAAATCGAAGATAGAG----- 1280
Qy 236 GlnLeuPheGlnGluTyrAspAsnHisIleLysSerSerValValGlySerGluArgLys 255
Db 1281 -----ATGGAAGAGACCCGACAGGACGAGTGCAGCAGAGCGGCCCAAGAACTGGCGCC 1334
Qy 256 ArgGlyMetGlnLeuGluAspLeuLysGlnGlnLeuGlnAlaGluGluAlaLeuVal 275
Db 1335 AAGCTCAGGTACCTCAGGATCAGCTGAGCCCGCTCACAAGGCAACGAGATACACGAGAG 1394
Qy 276 AlaLysGlnGluValIleAspLysLeuLysGluGluAla----- 288
Db 1395 AAGGAGATCCAGCGCTCAATAAGGCCCTTGAGGAGGCGCCTCAGCATCCAGGCTCTCCA 1454
Qy 289 -----GluGlnHis 291
Db 1455 TCATCTCGCGCTGACGCTTTTGGGAGTCCAGAAAGCGTGGGGGCCCATCTGAGGAAGCAG 1514
Qy 292 LysIleValMetGluThrValProValLeuLysAlaGlnAlaAspIleTyrLysAlaAsp 311
Db 1515 GAACCTAGTACACAGAAAT---GAGTTGCTGAAACACGAGGTTAAAGATCTTTGAAGAGGAC 1571
Qy 312 PheGlnAlaGluArgGlnAlaArgGluLysLeuAlaGluLysLysGluLeuLeuGlnGlu 331
Db 1572 TTCCAGAGGGAACCGAGTGAACCGTGAACGATGAATGAAGAGAGGAGGAGCTGAAGAAG 1631
Qy 332 GlnLeuGlnGlnLeuGlnArgGluTyr-----SerLysLeuLysAlaSerCys 347
Db 1632 CAAGTAGAAGAGTGGAGGCCCGCAGCTCACCTGACTAATGCCAGCTCAAAACTCTCAA 1691
Qy 348 GlnGluSerAlaArgIleGluAspMetArgLysArg----- 359
Db 1692 GAGGAGGAGGAGGCAAGGAAGCCCTCAAAACAGCAGAAAGAGGAAAGCAAGGCTTCGGGA 1751
Qy 360 -----HisValGlu-ValSerGlnAlaProLeuProPro----- 370
Db 1752 GAGCGCTACCATGGAACCCCAACCGCTGAGACGCTCTGGCGCGCTATCCCTATGCCCTAC 1811

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Qy 371 -----AlaProLaTyrLeuSerSerProLeuAlaLeuProSerGlnArgArgse 387
Db 1812 CCACCCATGCCAGCCATGGTACCTCACCAGTCCCTACAAGGACTGG-TCCCAGATCCGATA 1870
Qy 387 rProPro-----GluGluProProAep-----PheCy 396
Db 1871 CCCTCCACCCCTGTGCCCCATGGAGCACCGCGCCGCCACACCCCAACTCTCGCCTCTTCCA 1930
Qy 396 sCyProLeuCySerGlnTyrGlnAlaPro 405
Db 1931 TCTGCCGGAGTACACCTGGCGTCCACCC 1958

RESULT 8
US-08-875-435B-5
; Sequence 5, Application US/08875435B
; Patent No. 6593304
; GENERAL INFORMATION:
; APPLICANT: Hasegawa, Kazuhide
; APPLICANT: Arakawa, Emi
; APPLICANT: Oda, Shoji
; APPLICANT: Matsuda, Yuzuru
; APPLICANT: Takahashi, Katsuhito
; APPLICANT: Sugahara, Michihiro
; APPLICANT: Ishiyama, Haruo
; TITLE OF INVENTION: RECOMBINANT DNA COMPRISING DNA CODING
; TITLE OF INVENTION: FOR MYOSIN HEAVY CHAIN SM1 ISOFORM PROTEIN INSERTED INTO
; TITLE OF INVENTION: VECTOR DNA, MICROORGANISM CARRYING THE RECOMBINANT DNA, AND
; TITLE OF INVENTION: AN AGENT FOR TREATMENT OF ARTERIOSCLEROSIS COMPRISING THE
; TITLE OF INVENTION: RECOMBINANT DNA
; FILE REFERENCE: 07898-013001
; CURRENT APPLICATION NUMBER: US/08/875,435B
; CURRENT FILING DATE: 1997-07-25
; PRIOR APPLICATION NUMBER: PCT/JP96/00134
; PRIOR FILING DATE: 1996-01-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 6644
; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
US-08-875-435B-5

Alignment Scores:
Pred. No.: 6,19e-13 Length: 6644
Score: 237,00 Matches: 114
Percent Similarity: 40,20% Conservative: 83
Best Local Similarity: 23,27% Mismatches: 138
Query Match: 11,21% Indels: 155
DB: 4 Gaps: 21

US-09-377-795-2 (1-419) x US-08-875-435B-5 (1-6644)

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Db 2316 CATGGATGGGAGCAAGCCCTGTCATCTTCATGATCAAAAGCTCTGGAACCTGGACCCCAACTT 2375
Qy 21 -----AlaAlaPheGlnAepValLeu-----GlyGluGluSerProLeuGlyLys 35
Db 2376 GTACAGATCGGGCAGAGCAAAATCTTCTCCGACGCGGCGTCTGGCCCACTTGGAGGA 2435
Qy 36 ProAlaMetLeuHis-----Leu 41
Db 2436 GGAGCGGAGCTTGAAGATCACCGACGTCATCGCTTCAGGCCCTTCCAGGCCATGTGTCTGGCTA 2495
Qy 42 ProSerGluGlnGlyAla-----Pro 48
Db 2496 CCTCGCCCGCAGAGCCCTTCCCAAGCGCGCAGCAGCAGCTGACCGCCATGAAGTGTATCCA 2555
Qy 49 GluThrLeuGlnArgCysLeuGluGluAenGlnGluLeuArgAspAlaIle-ArgGlnSe 68
Db 2556 GAGGAAGTGGCGGC---CTACTGAAGCTGCGGAAGCTGCA---GTGGTGGCGC----- 2604
Qy 68 rAenGlnIleLeuArgGluArgCysGluGluLeuLeuHisPheGlnAlaSerGlnArgG1 88

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Db 2605 -----CTCTTCAACCAAGGTGAAGCCGCTGCTG-----CAGGTGACACGGCAGGA 2648
Qy 88 uGluLysGluPheLeuMetCysLysPheGlnGluAlaArgLysLeuValGluArgLeuG1 108
Db 2649 GGAGGAG-----ATGCAGGCCAAGAGGATGAGCTGCAGAAGATCAAGAGCGA----- 2697
Qy 108 yLeuGluLysLeuAspLeuLysArgGlnLysGluGlnAlaLeuArgGluValGluHisLe 128
Db 2698 -----CAGCAAGAGCGCGAGAGCGAGCTCCAGGAGCT 2729
Qy 128 uLysArgCysGlnGlnMetAlaGluAspLysAlaSerValLysAlaGlnVal----- 146
Db 2730 GCAGCAGAAGCACACAGCTGCTCCGAGGAGAAAGAACCTGCTGCAGGAGCAGCTGCAGGC 2789
Qy 147 -----ThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeuGluAlaThrLy 165
Db 2790 GGAGACGGAGCTGTACCGCGAGGCCGAGGAGATGCGCGTCCGCTGGCGGCCAAGAAGCA 2849
Qy 165 sGluCysGln-----AlaLeuGluGlyArgAlaArgAlaAlaSerGluGlnAl 181
Db 2850 GGAGCTGGAGGAAATCTGCTGATGATGAGGCGCCGCTGGAGGAGGAGGAAGACCGGG 2909
Qy 181 aArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAspG1 201
Db 2910 CCAGCAGCTGCAGCGCCGAGAGGAAGATGGCCAGCAGATGCTGGACCTGGAAGAGCA 2969
Qy 201 nLeu-----ArgMetGlnGlyGlnSerValGluAlaLe 213
Db 2970 ACTGGAGGAGGAGGAAGCTGCCAGGCAGAGCTACAGCTCGAAAAGGTCTACCGCCGAGGC 3029
Qy 213 uArgMetGluArg----- 217
Db 3030 CAAAGATCAAGAAGTTGGAGACCAACATCTCTGTCATGGACGATCAGAACCAACAGCTCTC 3089
Qy 218 -----GlnAlaAlaSe 221
Db 3090 AAAAGAGCGAAAACTCTCTGAAGAGAGGATTAGTATTAAACAACAAATCTTCCGAGGA 3149
Qy 221 rGluGluLysArgLys---LeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnG1 240
Db 3150 GGAAGAGAAGGCCCAAGCACTTGACCAAGCTGGAAGAACAAAGATGAATCATGATCTCAGA 3209
Qy 240 uTyrAspAenHisIleLysSerSerValValGlySerGluArg-----LysAr 256
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Qy 256 gGlyMet-----GlnLe 260
Db 3270 GAAGATGGACGCGAGGCCAGTGACCTCCACGAGCAGATCGCCGACCTCCAGCGCGCAGAT 3329
Qy 260 uGluAspLeuLysGlnGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVa 280
Db 3330 CGCAGAGCTCAAGATGCAGCTGGCCCAAGAGGAGAGGAGCTG-----CAGCGCGC 3380
Qy 280 lIleAspLysLeuLysGluAlaGluGlnHisLysIleValMetGluThrValProVa 300
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Qy 300 lLeuLysAlaGlnAlaAepIleTyrLysAlaAepPheGlnAlaGluArgGlnAlaArgG1 320
Db 3441 GCTGGAGGGGCACATCTCCGACCTGCAGGAGGACCTGGACTCAGAGCGGCGCCAGGAA 3500
Qy 320 uLysLeuAlaGluLysGluLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 336
Db 3501 CAAGGCCGAGAAGCAGACGAGCTGGGGGAGGAGCTGGAGGCGCTGAAGAGCGAGCT 3560
Qy 337 -----GlnArgG1 339
Db 3561 GGAGGACACGCTGGACACCGGCCACCGCAGGAGGAGCTCCGGGCCAAGCGGGAGGAGCA 3620
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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1776
; LENGTH: 7218
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1776

Alignment Scores:
Pred. No.: 4,9e-12 Length: 7218
Score: 228.50 Matches: 112
Percent Similarity: 40.55% Conservative: 81
Best Local Similarity: 23.53% Mismatches: 179
Query Match: 10.80% Indels: 104
DB: 4 Gaps: 19

US-09-377-795-2 (1-419) x US-09-949-016-1776 (1-7218)
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Qy 35 LysProAlaMetLeuHisLeuProSerGluGlnGlyAla-----ProGluThr 50
Db 1884 AGAACAGAGCGCTCCAGGGCCCTCCGCCACAGCTGGAGCAGCTAAGCAGTAGCTGAAGCA 1943
Qy 51 -LeuGlnArgCysLeuGluAenGlnGluLeuArgAspAlaIleArgGlnSerAsn-- 69
Db 1944 GAAGAGCGACGATTGAAGGAAGGTAGCGGAGACAGAGGCACTAGGAGGACCATGC 2003
Qy 70 -----GlnIleLeuArgGluArgCysGlu 78
Db 2004 CCAGCAACTGGCCACTGCTGCAGAGGAGCGAGGCCCTCTTAAGGAGCGGGATCGCGC 2063
Qy 78 uLeuLeuHisPheGlnAlaSerGlnArgGluGluLys-----GluPheLeuMetCy 95
Db 2064 TCTCAAGCAGCTGGAGGCACTGGAGAGGAGGAGAGGCTGGCCAAAGCTGGAGATTCTGCAGCA 2123
Qy 95 sLysPheGlnGluAlaArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeu 115
Db 2124 GCAACTTCAGTGGCTAATGAAGCCCGGACAGCTGCCAGCTCTAGTCACACAGGCCCA 2183
Qy 115 sArgGlnLysGluGlnAlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMe 135
Db 2184 GCGGAGAGGAGGAGGAGCTGAGCCGGAAGGTGGAGGAACCTCCAGGCCCTGTGTGAGACAGC 2243
Qy 135 tAlaGluAspLysAlaSerValLysAlaGlnValThrSerLeuLeuGlyGluGlnGln 155
Db 2244 CCGCCAGGAACAGCATGAGGCCCGCCAGCTTGCAGACTA-----GAGTTGCAGCT 2297
Qy 155 uSerGlnSerArgLeuGluAlaAlaThrLysGlu-----166
Db 2298 GCGGCTGCAGCAGCAAAAGCACTGAGAAAGAGAGGTTGGCCCGCAGGAGGACCAAGCT 2357
Qy 167 -----CysGlnAlaLeu-----Gln 171
Db 2358 CCAGAGCAGCTCCAGGCCCTCAAGAGTCTTGAAGGTCAACAGGGCAGCTTGAAGA 2417
Qy 171 uGlyArgAlaArgAlaAla-----SerGluGlnAlaArg-----GlnLeuGln 185
Db 2418 GGAGAGCGCAGGCGTGCAGATGCTTGAAGAGCAGCAGCGTGTGATCTCTGAGCTGAA 2477
Qy 185 uSerGluArgGluAlaLeuGlnGlnHisSer-----ValGlnValAspGlnLe 202
Db 2478 GCGAGAGACCGAGCCCTGGTGGAGAGCAGTAAAGCGGGAACGAAAGAGCTCGAAGAAGA 2537
Qy 202 uArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAlaSerGln 222
Db 2538 GAGGCGTGGCGCAAGGGCGTGGAGGCTCGATTACAGCAGCTTGGGGAGGCCCATCAGGC 2597
Qy 222 uGlu-----LysArgLysLeuAlaGlnLeuGlnValAlaTyrrHisGlnLeuPh 238
Db 2598 TGAGACTGAAGTCTCGCGGGAGCTGGCAGAGGCCCATGGCTGGCCAGCACAGCTGA 2657

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: February 9, 2005, 03:17:44 ; Search time 1630 Seconds  
(without alignments)  
1479.544 Million cell updates/sec

Title: US-09-377-795-2  
Perfect score: 2115  
Sequence: 1 MNRHLKSQLCENVPQSGP.....COYQAPDMDTLQIHVMECIE 419

Scoring table: BLOSUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0  
4313806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2\_1/USFIO\_spool/US09377795/runat\_07022005\_112552\_12179/app\_query.fasta\_1.583  
-DB=Published Applications NA -QFMT=fastap -SURFIX=p2n.rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US09377795 @CGN 1.1.628 @runat\_07022005\_112552\_12179  
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Database : Published Applications NA:  
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2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
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7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
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9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
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22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2115	100.0	1994	10	US-09-972-607-3 Sequence 3, Appli
2	2115	100.0	1994	10	US-09-851-673-1 Sequence 1, Appli
3	2115	100.0	1994	17	US-10-628-841-3 Sequence 3, Appli
4	2115	100.0	2009	18	US-10-761-370-1 Sequence 1, Appli
5	2115	100.0	2035	10	US-09-863-049A-3 Sequence 3, Appli
6	2105	99.5	1975	10	US-09-972-607-10 Sequence 10, Appl
7	2105	99.5	1975	17	US-10-628-841-10 Sequence 2, Appli
8	2028.5	95.9	2034	18	US-10-761-370-2 Sequence 4, Appli
9	1840.5	87.0	1104	14	US-10-792-063-4 Sequence 2, Appli
10	1822.5	86.2	1874	14	US-10-189-388-2 Sequence 8, Appli
11	1822.5	86.2	1874	17	US-10-408-305-2 Sequence 2, Appli
12	827	39.1	486	18	US-10-792-063-8 Sequence 8, Appli
13	756.5	35.8	483	18	US-10-792-063-6 Sequence 6, Appli
14	584.5	27.6	23106	10	US-09-863-049A-1 Sequence 1, Appli
C 15	443	20.9	2803	9	US-09-925-298-84 Sequence 84, Appl
C 16	443	20.9	2803	14	US-10-102-806-84 Sequence 11, Appl
17	436.5	20.6	1925	18	US-10-609-133-11 Sequence 13, Appl
18	436.5	20.6	2076	18	US-10-609-133-13 Sequence 9, Appli
19	430.5	20.4	2023	18	US-10-609-133-9 Sequence 1, Appli
20	420.5	19.9	1734	17	US-10-627-757-1 Sequence 3, Appli
21	420.5	19.9	1856	18	US-10-609-133-3 Sequence 5, Appli
22	420.5	19.9	2008	18	US-10-609-133-5 Sequence 1, Appli
23	420.5	19.9	2077	18	US-10-609-133-1 Sequence 128, App
24	420.5	19.9	2139	17	US-10-172-118-128 Sequence 128, App
25	420.5	19.9	2139	17	US-10-342-887-128 Sequence 79, Appl
26	420.5	19.9	2139	18	US-10-717-597-79 Sequence 213, App
27	420.5	19.9	2327	18	US-10-755-889-213 Sequence 17, Appl
28	416	19.7	1799	18	US-10-609-133-17 Sequence 69, Appl
29	414	19.6	1908	17	US-10-136-728-69 Sequence 71, Appl
30	411.5	19.5	1908	17	US-10-136-728-71 Sequence 15, Appl
31	410	19.4	1787	18	US-10-609-133-15 Sequence 12702, A
32	359	17.0	597	16	US-10-029-386-12702 Sequence 2339, Ap
33	357	16.9	236	10	US-09-918-995-2339 Sequence 26402, A
34	349	16.5	216	16	US-10-029-386-26402 Sequence 9902, Ap
35	334	15.8	526	16	US-10-029-386-9902 Sequence 23602, A
36	332	15.7	197	16	US-10-029-386-23602 Sequence 10, Appl
37	332	15.7	264	18	US-10-792-063-10 Sequence 1505, Ap
38	252	11.9	6354	15	US-09-917-800A-1505 Sequence 1780, Ap
39	251.5	11.9	15231	9	US-10-152-319A-1780 Sequence 35, Appl
40	251.5	11.9	15231	17	US-10-028-248A-35 Sequence 35, Appl
41	249	11.8	7396	17	US-10-107-782-35 Sequence 1601, Ap
42	249	11.8	7396	17	US-09-954-456-1601 Sequence 61, Appl
43	248.5	11.7	14800	9	US-10-269-909-61 Sequence 183, App
44	248.5	11.7	14800	16	US-10-717-597-183
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ALIGNMENTS

RESULT 1  
US-09-972-607-3  
; Sequence 3, Application US/09972607  
; Publication No. US20030105037A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; TITLE OF INVENTION: Antisense Modulation of Inhibitor-Kappa B Kinase-Gamma Expression  
; FILE REFERENCE: RTS-0191  
; CURRENT APPLICATION NUMBER: US/09/972,607  
; CURRENT FILING DATE: 2001-10-06  
; NUMBER OF SEQ ID NOS: 88  
; SEQ ID NO 3  
; LENGTH: 1994  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (149) ... (1408)  
US-09-972-607-3

Alignment Scores:  
 Pred. No.: 1.59e-172 Length: 2115.00  
 Score: 2115.00 Matches: 419  
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 DB: 10 Gaps: 0

US-09-377-795-2 (1-419) x US-09-972-607-3 (1-1994)

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QY 21 AlaAlaAspGlnAspValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40  
 DB 209 GCAGCAGATCAGGACGCTACTGGGGAAGAGTCTCTCTGGGAAGCCAGCCATGCTGCAC 268

QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluAsnGlnGlu 60  
 DB 269 CTGCTTTCAAGACAGGCGCTCTGAGACCTCCCTGAGACCTCCAGGAGGAGGAGGAGG 328

QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluLeuLeu 80  
 DB 329 CTCCGAGATGCCATCCGGCAGAGCACCAGATTTCTGGGAGCGCTGCAGGAGGTTCTG 388

QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGlu 100  
 DB 389 CATTTCCAAAGCCAGCCAGAGGAGGAGGAGGAGTCTCTCATGTGCAAGTTCCAGGAGGCC 448

QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGlu 120  
 DB 449 AGGAACTGTGTGAGAGACTCGGCTTGGAGAGCTCGATCTGAAGAGGAGGAGGAGGAG 508

QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140  
 DB 509 GCTCTGGGAGGTGGAGCACCTTGAAGAGATGCCAGCAGCAGATGGCTGAGGACAGGCC 568

QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnSerGlnSerArgLeu 160  
 DB 569 TCTGTGAAGCCAGGAGTGCCTCTTGTCTGGGAGCTGCGGAGCTGAGGAGGAGGAGGAG 628

QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180  
 DB 629 GAGGCTGCCACTAAGGATGCCAGGCTCTGAGGGTTCGGGCGCGGCGGCGGCGGAGGAG 688

QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200  
 DB 689 GCGCGGAGCTGGAGAGTGCAGCGGAGGCGCTGCAGCAGCAGCAGCAGCGTGCAGGTGCAC 748

QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220  
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QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240  
 DB 809 TCGAGGAGAGAGGAGGAGTGGCCAGTTGAGGTGGCTTATCACCAGCTCTTCCAGAA 868

QY 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260  
 DB 869 TAGCAACACCATCAAGAGCAGCGTGTGGGAGTGCAGCGGAGGAGGAGGAGGAGGAGG 928

QY 261 GluAspLeuLysGlnGlnLeuGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280  
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QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300  
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QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320

DB 1049 CTGAAGGCGGCGGATATCTTACAAGCGGAGTCTTCAAGCGGAGTTCAGGCGAGGCCGCCGAG 1108

QY 321 LysLeuAlaGluLysLysGluLeuGlnGluLeuGlnGlnLeuGlnArgGluTyr 340

DB 1109 AAGCTGGCGGAGAGAGAGCTCTCTGAGGAGCAGCTGGAGCAGCTGCAGAGGAGTAC 1168

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DB 1169 AGCAAACTGAAGGCGGAGTGTCTGAGGTCGCGCAGGATCGAGGACATGAGGAAGCGCAT 1228

QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380

DB 1229 GTCGAGGTCCTCCAGGCGCCCTTGGCCCCCGCTGCTCTCTCTCTCTCTCTCTCTCTCT 1288

QY 381 LeuProSerGlnArgSerProGluGluProProAspPheCysCysProLysCys 400

DB 1289 CTGCGCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1348

QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419

DB 1349 CAGTATCAGGCGCTGATATGACACCTCTGAGATACATGTCTGAGTGCATTGAG 1405

RESULT 2  
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 ; Sequence 1, Application US/09851673  
 ; Publication No. US20030165985A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Derry, Jonathan  
 ; APPLICANT: Fanslow, William  
 ; APPLICANT: Dougall, William  
 ; TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40 SIGNALING  
 ; FILE REFERENCE: 3198  
 ; CURRENT APPLICATION NUMBER: US/09/851.673  
 ; CURRENT FILING DATE: 2001-05-08  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1994  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (149)..(1405)  
 US-09-851-673-1

Alignment Scores:  
 Pred. No.: 1.59e-172 Length: 1994  
 Score: 2115.00 Matches: 419  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 10 Gaps: 0

US-09-377-795-2 (1-419) x US-09-851-673-1 (1-1994)

QY 1 MetAsnArgHisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
 DB 149 ATGATAGGACCTCTCGAAGAGCCAACTGTGTGAGATGGTGGAGCCAGTGTGGCCCG 208

QY 21 AlaAlaAspGlnAspValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40  
 DB 209 GCAGCAGATCAGGACGCTACTGGGGAAGAGTCTCTCTGGGAAGCCAGCCATGCTGCAC 268

QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluAsnGlnGlu 60  
 DB 269 CTGCTTTCAAGACAGGCGCTCTGAGACCTCCCTGAGACCTCCAGGAGGAGGAGGAGGAGG 328

QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluLeuLeu 80  
 DB 329 CTCCGAGATGCCATCCGGCAGAGCACCAGATTTCTGGGAGCGCTGCAGGAGGTTCTG 388

QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGlu 100



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Db 389 CATTTCCAGCCAGCCAGGAGGAGGAGGAGTTCCTCATGTGCAAGTTCCAGGAGGCC 448
Qy 101 ArgLysLeuValGluArgLeuGlyLeuGlyLeuAspLeuLysArgGlnLysGluGln 120
Db 449 AGGAACCTGGTGGAGAGACTCGGCTCGAGAAAGCTCGATCTGAAGAGCGAAGAGGACG 508
Qy 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140
Db 509 GCTCTCGGGAGGTGGAGCACCTCAAGAGATGCCAGCAGCAGATGGCTGAGGACAAGGCC 568
Qy 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerArgLeu 160
Db 569 TCTGTGAAGCCAGGTGACGCTCTGCTCGGGAGCTGCAGGAGCCAGCAGTCGCTTG 628
Qy 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
Db 629 GAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGTCGGGCCCGGGCGGCAGGAGCAG 688
Qy 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
Db 689 GCGCGGAGCTGGAGAGTGAAGCGAGCGCTGCAGCAGCAGCAGCAGCGTGCAGGTGAC 748
Qy 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
Db 749 CAGCTGCGCATGCGAGGCGCAGAGCGTGGAGCGCGCTCCGCATGGAGCGCCAGCGGCC 808
Qy 221 SerGluLysArgLysLeuAlaGlnLeuGlnValAlaAlaTyrHisGlnLeuPheGlnGlu 240
Db 809 TCGAGAGAGAAGAAAGCTGGCCAGTTGCGAGGTGGCTTATCACCAAGCTCTTCCAAGAA 868
Qy 241 TyrAspAsnHisIleLysSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
Db 869 TACGACAAACACATCAAGAGCAGCGTGTGGCGAGTGCAGCGAAGCCGAGGATGCAGCTG 928
Qy 261 GluAspLeuLysGlnLeuGlnGlnAlaGluAlaLeuValAlaLysGlnGlnVal 280
Db 929 GAAGATCTCAACAGCAGCTCCAGCAGCGCGAGGAGGCCCTGTGTGGCCAAACAGGAGGTG 988
Qy 281 IleAspLysLeuLysGluAlaGluGlnHisLysIleValMetGluThrValProVal 300
Db 989 ATCGATAGCTGAAGGAGGAGCGCCAGCAGCAGCAAGATTGTGATGGAGACCGTTCCGGTG 1048
Qy 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
Db 1049 CTGAAGCCCGAGCGGATATCTACAAGCGGACTTCCAGGCTGAGAGCGAGCCCGGGAG 1108
Qy 321 LysLeuAlaGluLysLysGluLeuGlnGlnGlnLeuGlnLeuGlnArgGluTyr 340
Db 1109 AAGCTGGCCGAGAAAGAGGAGCTCTGCAGAGCAGCTGGAGCAGCTGCAGAGGAGTAC 1168
Qy 341 SerLysLeuLysAlaSerCysGlnGluSerAlaArgIleGluAspMetArgLysArgHis 360
Db 1169 AGCAACTGAAGGCCAGCTGTCAAGAGTGCGCCAGGATCCAGGACATGAGAGAGCGCAT 1228
Qy 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380
Db 1229 GTCGAGGTCTCCAGGCCCTTGGCCCGCCCTGCTACCTCTCTCTCTCCCTTGCC 1288
Qy 381 LeuProSerGlnArgArgSerProGluProGluProAspPheCysCysProLysCys 400
Db 1289 CTGCCAGCCAGAGGAGGAGCGCCCGCCGAGGAGCCACTGACTTCTGCTGCCAAGTGC 1348
Qy 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
Db 1349 CAGTATCAGGCCCTGTATGGACACCTCGAGATACATGTCTATGGAGTGCATTTAG 1405
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## RESULT 3

US-10-628-841-3

; Sequence 3, Application US/10628841

; Publication No. US20040023918A1

; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia

; APPLICANT: Jacqueline Wyatt

```
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-GAMMA EXPRESSION
; FILE REFERENCE: RTS-0191
; CURRENT APPLICATION NUMBER: US/10/628,841
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/972,607
; PRIOR FILING DATE: 2001-10-06
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 1994
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (149)...(1408)
; US-10-628-841-3
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## Alignment Scores:

Pred. No.:	1,59e-172	Length:	1994
Score:	2115.00	Matches:	419
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	17	Gaps:	0

US-09-377-795-2 (1-419) x US-10-628-841-3 (1-1994)

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Qy 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
Db 149 ATGAATAGGCACCTCTGGAGAGCCCAACTGTGTGAGATGTCGAGCCCGAGTGTGGCCCG 208
Qy 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40
Db 209 GCAGCAGATCAGACGCTACTTGGCGGAGAGTCTCTCTCTGGGGAAGCCAGCCATGCTGCAC 268
Qy 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGlnAsnGlnGlu 60
Db 269 CTGCTTTCAAGACAGGCGCTCTCTGAGACCTCCAGCGCTGCTGGAGGAGATCAAGAG 328
Qy 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluLeuLeu 80
Db 329 CTCGAGATGTCATCCGGCAGAGCAACCAAGATTCTCGGAGAGCGCTGCGAGGAGCTTCTG 388
Qy 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
Db 389 CATTTCCAGCCAGCCAGAGGAGGAGAGGAGTCTCTCATGTGCAAGTTCAGAGAGGCC 448
Qy 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
Db 449 AGGAAACTGGTGGAGAGACTTCGGGCTTCGAGAAAGCTCGATCTGAAGAGGCGAAGAGGACG 508
Qy 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140
Db 509 GCTCTCGGGAGGTGGAGCACCTGGAAGAGATGCCAGCAGCAGATGGCTGAGGACAAGGCC 568
Qy 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160
Db 569 TCTGTGAAGCCAGGTGAGCTCTTGTCTCGGGAGCTGCAGGAGGAGCCAGATCGCTTG 628
Qy 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
Db 629 GAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGTCGGGCCCGGGCGGCAGGAGCAG 688
Qy 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
Db 689 GCGCGCAGCTGGAGAGTGAAGCGAGCGCTGCAGCAGCAGCAGCAGCGTGCAGGTGAC 748
Qy 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
Db 749 CAGCTGCGCATGCGAGGCGCAGAGCGTGGAGGCCCGCTCCGCATGGAGCGCCAGCGGCC 808
Qy 221 SerGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240
Db 809 TCGGAGAGAGAAGAAAGCTGGCCAGTTGCGAGGTGGCTTATCACCAAGCTCTTCCAAGAA 868
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QY 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260  
Db 869 TACGACAAACCAATCAAGAGAGCGTGTGGCAGTGCAGCGAAGCGAGGAATGCAGCTG 928  
QY 261 GluAspLeuLysGlnGlnLeuGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280  
Db 929 GAGATCTCAACAGCAGCTCCAGAGCCGAGAGGCCCTGTGTGCCAAACAGGAGGTG 988  
QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300  
Db 989 ATCGATAAGCTGAAGGAGGAGCGCAGCAGCAAGATTGTGATGAGACCGTTCGGGTG 1048  
QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320  
Db 1049 CTGAAGGCCCAAGGCGGATATCTACAGGCGACTTCCAGGCTGAGAGGCGCGCGGAG 1108  
QY 321 LysLeuAlaGluLysGluLeuLeuGlnGlnLeuGlnGlnLeuGlnArgGluTyr 340  
Db 1109 AAGCTGCCGAGAGAAGAGGAGCTCTGCAGAGCAGCTGGAGCAGCTGCAGAGGAGTAC 1168  
QY 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysArgHis 360  
Db 1169 AGCAAACTGAAGCGCAGCTGTGAGGAGTCGCCCAGGATCGAGGACATGAGGAAGCGCAT 1228  
QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaProAlaTyrLysSerSerProLeuAla 380  
Db 1229 GTGAGGTCTCCAGGCCCTTGGCCCCCGCCCTGCTACTCTCTCTCCCTGGCC 1288  
QY 381 LeuProSerGlnArgArgSerProGluGluProGluGluProAspPheCysCysProLysCys 400  
Db 1289 CTGCCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1348  
QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419  
Db 1349 CAGTATCAGGCCCTGATATGAGACCCCTGCAGATACATGTGATGAGTGCATTGAG 1405

## RESULT 4

US-10-761-370-1  
; Sequence 1, Application US/10761370  
; Publication No. US20040219615A1  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR F  
; TITLE OF INVENTION: AND OTHER PROTEINS  
; FILE REFERENCE: WALLACH-27  
; CURRENT APPLICATION NUMBER: US/10/761,370  
; CURRENT FILING DATE: 2004-01-22  
; PRIOR APPLICATION NUMBER: US/09/646,403  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: IL 123758  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: PCT/IL99/00158  
; PRIOR FILING DATE: 1999-03-18  
; PRIOR APPLICATION NUMBER: IL 126024  
; PRIOR FILING DATE: 1998-09-01  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 1  
; LENGTH: 2009  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-761-370-1

Alignment Scores:  
Pred. No.: 1,61e-172 Length: 2009  
Score: 2115.00 Matches: 419  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 18 Gaps: 0

US-09-377-795-2 (1-419) x US-10-761-370-1 (1-2009)

QY 1 MetAsnArgHisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
Db 154 ATGATATAGCACCCTCTGGAAGAGCCACTGTGTGAGATGGTCAGCCCATGTGTGCCCCG 213  
QY 21 AlaAlaAspGlnAspValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40  
Db 214 GCAGCAGATCAGGACGTACTGGCGAAGAGTCTCTCTCTGGGGAAGCCAGCCATGTCTGCAC 273  
QY 41 LeuProSerGluGlnGlnValAlaProGluThrLeuGlnArgCysLeuGluGlnGlnGlu 60  
Db 274 CTGCCTTTCAGAAACAGGGCGCTCTGAGACCCCTCCAGCGCTGCTGAGGAGGAATCAAGAG 333  
QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGlnLeuLeu 80  
Db 334 CTCGAGATGTCATCCGCGCAGACCAACAGATTCTGCGGAGAGCGTTCGAGAGGCTTCTG 393  
QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100  
Db 394 CATTTCCAAAGCCAGCCAGAGGAGGAGAGGAGTTCCTCATGTGCAAGTTCCAGGAGGCC 453  
QY 101 ArgLysLeuValGluArgLeuGlyLeuGlyLysLeuAspLeuLysArgGlnLysGlnGln 120  
Db 454 AGGAACCTGGTGGAGAGACTCGGCTTGGAGAGGCTCGATCTGAAGAGGAGGAGGAGGAG 513  
QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140  
Db 514 GCTCTCGGGAGGTGGAGCACTGAAGAGATGCCAGCAGCAGATGGCTGAGGACAAAGGCC 573  
QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160  
Db 574 TCTGTGAAAGCCAGGTGACGTCTTCTGTCGGGAGGCTGCAGGAGGAGCAGAGTGCCTG 633  
QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGluArgAlaArgAlaAlaSerGluGln 180  
Db 634 GAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGGTTCGGGCCCGGCGGCGGAGGAGGAG 693  
QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200  
Db 694 GCGCGCAGCTGGAGAGTGCAGCGCGCTGCAGCAGCAGCAGCAGCAGCTGCAGGTGCAG 753  
QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220  
Db 754 CAGCTGCGCATGACAGGCGCAGAGGCTGGAGCGCGCTCCGCATGGAGCGGCGGCGGCG 813  
QY 221 SerGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240  
Db 814 TCGGAGGAGAGAGGAGAGTGGCCACTTGCAGGTGGCTATCACAGCTCTTCCAGAA 873  
QY 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260  
Db 874 TACGACAAACCAATCAAGAGCAGCGTGTGGCAGTGCAGCGGAAGCGGAGGAATCAGCTG 933  
QY 261 GluAspLeuLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280  
Db 934 GAGATCTCAACAGCAGACTCCAGAGCGGAGGAGGCGCTGGTGGGCGCAACAGAGAGGTG 993  
QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300  
Db 994 ATCGATAAGCTGAAGGAGGAGGCGCGAGCAGCAGCAAGATTGTGATGAGAGCCGTTCCG 1053  
QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320  
Db 1054 CTGAAGGCCCAGGCGGATATCTACAGGCGGACTTCCAGGCTGAGAGGCGGCGGAG 1113  
QY 321 LysLeuAlaGluLysGluLeuLeuGlnGlnGlnLeuGlnGlnLeuGlnArgGluTyr 340  
Db 1114 AAGCTGCCGAGAGAAGGAGGCTCTCTGCAGAGCAGCTGCAGGAGGAGTAC 1173  
QY 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysArgHis 360  
Db 1174 AGCAAACTGAAGGCCAGCTGTGAGGAGTGGCCAGGATCGAGGACATGAGGAGCGCAT 1233



; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-GAMMA EXPRESSION

; FILE REFERENCE: RTS-0191  
; CURRENT APPLICATION NUMBER: US/09/972,607  
; CURRENT FILING DATE: 2001-10-06  
; NUMBER OF SEQ ID NOS: 88  
; SEQ ID NO 10  
; LENGTH: 1975  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (111) ... (1370)  
US-09-972-607-10

Alignment Scores:  
Pred. No.: 1,14e-171 Length: 1975  
Score: 2105.00 Matches: 417  
Percent Similarity: 99.52% Conservative: 0  
Best Local Similarity: 99.52% Mismatches: 2  
Query Match: 99.53% Indels: 0  
DB: 10 Gaps: 0

US-09-377-795-2 (1-419) x US-09-972-607-10 (1-1975)

QY 1 MetAsnArgHisLeuTrrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
DB 111 ATGAATAGGCACCTCTGGAGAGCCCACTGTGTGAGATGGTCAGGCCCACTGGTGGCCCG 170  
QY 21 AlaAlaSerGlnAspValLeuGlyGluGluSerProLeuGlyProAlaMetLeuHis 40  
DB 171 GCACGAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGGAAGCCAGCCATGCTGCAC 230  
QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluGlnGlu 60  
DB 231 CTGCCTTCAGAACAGGCGCTCTGAGACCCCTCAGCGCTGCGGAGAGGAATCAAGAG 290  
QY 61 LeuArgAspAlaLeuArgGlnSerAsnGlnLeuLeuArgGluArgCysGluGluLeu 80  
DB 291 CTCGAGATGCCATCCGGCAGAGCAACCAAGATTCCTGGGAGGCGTTCGAGAGCTTCTG 350  
QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100  
DB 351 CATTTCCAAAGCCAGCAGAGGAGGAGAGAGGAGTCTCTCATGTGCAAGTTCAGAGGCC 410  
QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysGlnLysGluGln 120  
DB 411 AGGAACTGTGTGAGAGACTCGGCTGGAGAGCTCGATCTGAGAGGCGAGAGGAGCAG 470  
QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140  
DB 471 GCTCTGGGAGGTGGAGCACCTGAAAGAGATGCCAGCAGCAGATGGCTGAGGACAAGGCC 530  
QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160  
DB 531 TCTGTGAACCCAGGTGAGTACCTTGTCTGGGAGGCTGCGAGAGGACGAGTGCCTTG 590  
QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180  
DB 591 GAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGCTCGGGCCCGGCGCCAGCGAGCAG 650  
QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200  
DB 651 GCSCGGCAGCTGAGAGTGGCGGAGGCGCTGCGAGCAGCAGCAGCAGCAGCGTGCAGTGGAC 710  
QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220  
DB 711 CAGCTGGCATGAGGCGCCAGAGCGTGGAGGCGCGCTCCGATGGAGCGCCAGCGCCGCC 770  
QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240  
DB 771 TCGGAGGAGAGAGGAAGTGGCCAGTTGCGAGTGGCGCTATCACCAGCTCTTCCAGAA 830  
QY 241 TyrAspAsnHisIleLysSerValValGlnSerGluArgLysArgGlyMetGlnLeu 260

DB 831 TACGCAACCAACCATCAAGAGCAGCGCTGTGGCAGTGGCGAAGCGAGGAATGCAGCTG 890  
QY 261 GluAspLeuLysGlnGlnGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280  
DB 891 GAAGATCTCAACACAGCAGCTCCAGCAGCGCAGGAGGCGCTGTGGCCAAACAGGAGGTG 950  
QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisIleValMetGluThrValProVal 300  
DB 951 ATCGATAAGCTGAAGGAGGAGCGCCAGCAGCAGCAAGATTGTGATGAGACCGTTCGGGTG 1010  
QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320  
DB 1011 CTGAAGGCCCGAGCGGATATCTACAAGCGGACTTCCAGGCTGAGAGGCGAGGCCGCGAG 1070  
QY 321 LysLeuAlaGluLysGluLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 340  
DB 1071 AAGCTGGCCGAGAGAGAGGCTCTCTGAGAGGAGCTGGAGCAGCTGCAGAGGAGGTAC 1130  
QY 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysArgHis 360  
DB 1131 AGAAACTGAAGGCCAGCTGTCTCAGAGTCCGCGCAGGATCGAGGACATGAGGAAGCGCAT 1190  
QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380  
DB 1191 GTCAGAGTCTCCAGGCCCCCTTGGCCCCCGCCCTGCTTCTCTCTCTCTCTCTCTCTCT 1250  
QY 381 LeuProSerGlnArgArgSerProGluGluProGluProAspPheCysCysProLysCys 400  
DB 1251 CTGCCCAGTCAGAGGAGGAGGCCCGCCAGAGGAGCCACTGACTTCTGTCTCCCAAGTGC 1310  
QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419  
DB 1311 CAGTATCAGGCCCTGATATGACACCCCTGACAGATACATGTGATGAGTGCATTGAG 1367

#### RESULT 7

US-10-628-841-10  
; Sequence 10, Application US/10628841  
; Publication No. US20040023918A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-GAMMA EXPRESSION  
; FILE REFERENCE: RTS-0191  
; CURRENT APPLICATION NUMBER: US/10/628,841  
; CURRENT FILING DATE: 2003-07-28  
; PRIOR APPLICATION NUMBER: US/09/972,607  
; PRIOR FILING DATE: 2001-10-06  
; NUMBER OF SEQ ID NOS: 88  
; SEQ ID NO 10  
; LENGTH: 1975  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (111) ... (1370)  
US-10-628-841-10

Alignment Scores:  
Pred. No.: 1,14e-171 Length: 1975  
Score: 2105.00 Matches: 417  
Percent Similarity: 99.52% Conservative: 0  
Best Local Similarity: 99.52% Mismatches: 2  
Query Match: 99.53% Indels: 0  
DB: 17 Gaps: 0

US-09-377-795-2 (1-419) x US-10-628-841-10 (1-1975)

QY 1 MetAsnArgHisLeuTrrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
DB 111 ATGAATAGGCACCTCTGGAGAGCCCACTGTGTGAGATGGTCAGGCCCACTGGTGGCCCG 170  
QY 21 AlaAlaSerGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40

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Db 171 GCAGCAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGGAAGCCAGCCATGCTGCAC 230
Qy 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluAenGlnGlu 60
Db 231 CTGCCTTTCAAGAACAGGCGCTCTCTGAGACCCCTCCAGCGCTGCTGGAGGAGNAATCAAGAG 290
Qy 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80
Db 291 CTCCGAGATGCCATCCGCGCAGAGCAACAGATTCTGGGGAGCGCTCGGAGGAGCTTCTG 350
Qy 81 HisPheGlnAlaSerGlnArgGluGluGlyPheLeuMetCysLysPheGlnGluAla 100
Db 351 CATTTCCAAGCCAGCAGAGGAGGAGAGAGTCTCTCATGTGCAAGTTCCAGAGGCC 410
Qy 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
Db 411 AGGAACTGTGGAGAGACTCGGCTCGGAGAGCTCGATTCTGAAGAGCGCAGAGGAGCAG 470
Qy 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140
Db 471 GCTCTCGGGAGGTGGAGCACCTGAAGAGATGCCAGCAGCAGATGGCTGAGGACNAGGCC 530
Qy 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerArgLeu 160
Db 531 TCTGTGAAGCCAGGTGAGCTCTCTGCTCGGGAGCTGCAGGAGAGCCAGAGTCGCTTG 590
Qy 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
Db 591 GAGGCTGCCACTAAGGAATGCCAGGCTCTGAGGGTTCGGCCCGGGCGCCAGCAGAGCAG 650
Qy 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
Db 651 GCGCGGAGCTGGAGAGTGGAGCGGAGCGCTGCAGCAGCAGCAGCACAGCTGCGAGTGGAC 710
Qy 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
Db 711 CAGCTGCGCATGCAGGCCAGAGCGTGTGGCAGTGGCGCGCTCGCATGGAGCGCCAGCGGCC 770
Qy 221 SerGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240
Db 771 TCGAGAGAGAGAGAGAGTGGCGCCAGTTGACGTGGTGGCTTATCACCAAGCTCTTCCAAGAA 830
Qy 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
Db 831 TAGCACAACACATCAAGACAGCGTGTGGCAGTGGAGCGGAGCGAGGAGATTCGAGCTG 890
Qy 261 GluAspLysLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280
Db 891 GAAGATCTCAAAACAGCAGCTCCAGCAGCGCGAGAGCGCTGTGGTGGCCAAACAGGAGGTG 950
Qy 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300
Db 951 ATCGATAAGCTGAAGGAGGAGGCGGAGCAGCAGCAAGATTGTGATGGAGACCGTTCCGGTG 1010
Qy 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
Db 1011 CTGAGGCCCAGCGGATATCTACAGCGGACTTCCAGGCTGAGAGGCGAGGCCGGGAG 1070
Qy 321 LysLeuAlaGluLysLysGluLeuLeuGlnGlnLeuGlnLeuGlnArgGluTyr 340
Db 1071 AAGCTGGCCGAGAAGAAGAGAGTCTCTGCAGGAGCAGCTGGAGCAGCTGCAGAGGGAGTAC 1130
Qy 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysArgHis 360
Db 1131 AGAAACTGAAGCCAGCTGTCAAGAGTTCGGCCAGGATCGAGGACATGAGGAAGCGGCAT 1190
Qy 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380
Db 1191 GTGAGGTCTCCAGGCCCTTGGCCCCCGCCCTTGCCTTCTCTCTCCCTTGGCC 1250
Qy 381 LeuProSerGlnArgArgSerProProGluGluProProAspPheCysCysProLysCys 400
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Db 1251 CTGCCAGTCAGAGGAGGAGGCCCCCAGAGAGCCACCTGCTGCTGTCCCAAGTGC 1310
Qy 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
Db 1311 CAGTATCAGGCCCCCTGATATGGAACCCCTGCAGATACATGTCATGGAGTCATTGAG 1367

RESULT 8
US-10-761-370-2
; Sequence 2, Application US/10761370
; Publication No. US20040219615A1
; GENERAL INFORMATION:
; APPLICANT: KOVALENKO, Andrei
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR P
; FILE REFERENCE: WALLACH-27
; CURRENT APPLICATION NUMBER: US/10/761,370
; PRIOR FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: US/09/646,403
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: IL 123758
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: PCT/IL99/00158
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: IL 126024
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-761-370-2

Alignment Scores:
Pred. No.: 4,57e-165 Length: 2034
Score: 2028.50 Matches: 413
Percent Similarity: 97.64% Conservative: 0
Best Local Similarity: 97.64% Mismatches: 6
Query Match: 95.91% Indels: 4
DB: 18 Gaps: 1

US-09-377-795-2 (1-419) x US-10-761-370-2 (1-2034)
Qy 1 MetAsnArgHisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
Db 172 ATGAATAGGCACCTCTGGGAAGAGCCAACTGTGTGAGATGGTGCAGCCCACTGGTGGCCCG 231
Qy 21 AlaAlaAspGlnAspValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40
Db 232 GCAGCAGATCAGGACGCTACTGGGCGAAGAGTCTCTCTGGGGAAGCCAGCCATGCTGCAC 291
Qy 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGlnGlnG 60
Db 292 CTGCCTTCAGAACAGGCGCTCTCTGAGACCTCCAGCGCTGCTGGAGGAGAATCAAGA 351
Qy 60 uLeuArgAspAlaIleArgGln-SerAsnGlnIleLeuArgGluArgCysGlu---GluL 79
Db 352 GCTCCAGAGTGCATCCGCGAGTAGCAACACAGATTCTTCGGGAGCTGCGGNAGGGAGCT 411
Qy 79 euleuHis-PheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGln 98
Db 412 TTCTGATTTTCCNAGCCAGCCAGAGGAGGAGAGGAGTTCCTCATGTGCATGTTCCAG 471
Qy 99 GluAlaArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLys 118
Db 472 GAGGCAGGAAACTGGTGCAGAGACTCGCGCTCGAGAAAGCTCGATCTGAAGAGGAGCAAG 531
Qy 119 GluGlnAlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAsp 138
Db 532 GAGCAGGCTCTCGCGGAGGTGGAGCACCTCAAGAGATGCCAGCAGCAGATGGCTGAGGAC 591
Qy 139 LysAlaSerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGluSerGlnSer 158
```

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Db 592 AAGCCCTCTGGAAGCCCGAGGTACGCTCTGCTGGGGAGCTGCAGGAGCCAGAGT 651
Qy 159 ArgLeuGluAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaAlaSer 178
Db 652 CGCTTGGAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGCTGGGCCCGGGCCAGC 711
Qy 179 GluGlnAlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnHisSerValGln 198
Db 712 GAGCAGCGCGGCGAGCTGGAGAGTGAAGCGAGCGCTGCAGCAGCAGCACAGCGTGCAG 771
Qy 199 ValAspGlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGln 218
Db 772 GTGACACAGCTGCCATGCGAGGCCAGAGCTGGAGCCGCTCCGCGATGAGGCGCCAG 831
Qy 219 AlaAlaSerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaThrHisGlnLeuPhe 238
Db 832 CGCGCCTCGGAGGAGAGAGAGTGGCCAGTTCAGGTGGCTTATCACAGCTCTTC 891
Qy 239 GlnGluTyrAspAsnHisLysSerValValGlySerGluArgLysArgGlyMet 258
Db 892 CAAGAATACGACACACACATCAAGAGCAGCGTGGTGGCGAGTGAGCGGAAGCGAGGAATG 951
Qy 259 GlnLeuGluAspLeuLysGlnGlnLeuGlnAlaGluGluAlaLeuValAlaLysGln 278
Db 952 CAGCTGGAAGATCTCAACACAGCAGCTCCAGAGCGCGAGAGGCCCTGGTGGCCAAACAG 1011
Qy 279 GluValLysLeuLysGlnGluAlaGluGlnHisLysLeuValMetGluThrVal 298
Db 1012 GAGGTGATCGATAAGCTGAAGGAGGAGGCGCGAGCAGCACAGATTGTGATGAGACCGTT 1071
Qy 299 ProValLeuLysAlaGlnAlaAspLeuTyrLysAlaAspPheGlnAlaGluArgGlnAla 318
Db 1072 CCGGTGCTGAAGCCCGGCGGATATCTACAGGCGGACTTCAGGCTGAGAGGCGAGGCC 1131
Qy 319 ArgGluLysLeuAlaGluLysGlnLeuLeuGlnGlnGlnLeuGlnGlnArg 338
Db 1132 CGGAGAGAAGCTGGCCGAGAAGAGGAGCTCTGTCAGAGCAGCTGGAGCAGCTGCAGAGG 1191
Qy 339 GluTyrSerLysLeuLysAlaSerCysGlnGluSerAlaArgIleGluAspMetArgLys 358
Db 1192 GAGTACAGCAAACTGAAGCGCAGCTGTCAAGAGTCCGCCAGGATCGGCCAGATGAGGAAG 1251
Qy 359 ArgHisValGluValSerGlnAlaProLeuProAlaProAlaProAlaTyrLeuSerPro 378
Db 1252 CGGCATGTCAGCTCTCCAGGCCCTTGGCCCCCGCCCCCTGCTTCTCTCTCCC 1311
Qy 379 LeuAlaLeuProSerGlnArgSerProProGluGluProProAspPheCysPro 398
Db 1312 CTGGCCCTGCCCAGCAGAGGAGGAGGCCCGCCCGAGGAGCCACCTGACTTCTGTCTCCC 1371
Qy 399 LysCysGlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIle 418
Db 1372 AAGTGCCAGTATCAGGCCCCCTGATATGGACACCCCTGCAGATACATGTATGAGTGCATT 1431
Qy 419 Glu 419
Db 1432 GAG 1434
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## RESULT 9

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US-10-792-063-4
; Sequence 4, Application US/10792063
; Publication No. US20040175797A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jason
; APPLICANT: Garrett-Engle, Phillip
; APPLICANT: Kan, Zhengyan
; TITLE OF INVENTION: IKBG
; FILE REFERENCE: R03-011-208PV
; CURRENT APPLICATION NUMBER: US/10792,063
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 06/452,293
; PRIOR FILING DATE: 2003-03-04
```

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; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-792-063-4

Alignment Scores:
Pred. No.: 3,4e-149 Length: 1104
Score: 1840.50 Matches: 368
Percent Similarity: 87.83% Conservative: 0
Best Local Similarity: 87.83% Mismatches: 0
Query Match: 87.02% Indels: 51
DB: 18 Gaps: 1

US-09-377-795-2 (1-419) x US-10-792-063-4 (1-1104)

Qy 1 MetAsnArgHisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
Db 1 ATGAATAGGCACCTCTGGAGAGCCAACTGTGTGAGATGGTGCAGCCACAGTGGTGGCCCG 60
Qy 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40
Db 61 GCAGCAGATCAGGACGTAATCTGGCGAAGAGTCTCTCTGGGGGAAGCCAGCATGCTGCAC 120
Qy 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60
Db 121 CTGCCTTCAGAAACAGGCGCTCTTGAGACCTCCAGCGCTCCCTGGAGGAGGAATCAAGAG 180
Qy 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeu 80
Db 181 CTCGAGATGTCATCCGCGCAGAGCAACAGATTCCTCGCGGAGCGCTGGAGAGGCTTCTG 240
Qy 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
Db 241 CATTTCCAGCCAGCCAGGAGGAGGAGAGAGGATTCCTCATGTGCAGTTCAGAGAGGCC 300
Qy 101 ArgLysLeuValGluArgLeuGlyLeuGlyLysLeuAspLeuLysArgGlnLysGln 120
Db 301 AGGAAACTGGTGGAGAGACTCGGCTCGGAGAGCTCGATCTGAAGAGGCGAGAGGAGCAG 360
Qy 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140
Db 361 GCTCTGGGAGGTTGGAGACCTGAAGATGCCAGCAGCAGATGCTGAGAGCAAGGCC 420
Qy 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGluSerGlnSerArgLeu 160
Db 421 TCTGTAAAGCCAGGTGACGCTCTTCTCGGGAGCTGCAGGAGAGCCAGAGTGCCTTG 480
Qy 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
Db 481 GAGCTCCCACTAAGGAATCCAGGCTCTGAGGCTCGG----- 519
Qy 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnHisSerValGlnValAsp 200
Db 519 ----- 519
Qy 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220
Db 519 ----- 519
Qy 221 SerGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240
Db 520 -----AGGAAGCTGGGCCAGTTGAGGTGGCCTATCACCAGCTCTTCCAGAA 567
Qy 241 TyrAspAsnHisLysSerSerValValCysSerGluArgLysArgGlyMetGlnLeu 260
Db 568 TAGCACAACACATCAAGACAGCGTGGTGGCAGTGCAGCGGAAGCCAGGAATGCAGCTG 627
Qy 261 GluAspLeuLysGlnGlnLeuGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280
Db 628 GAAGATCTCAACAGCAGCTCCAGCAGCGCGGAGGAGGCCCTGGTGGCCAAACAGAGGCTG 687
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; Publication No. US2003022867A1
; GENERAL INFORMATION:
; APPLICANT: SHOJI, YAMAKA
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCE ENCODING A MODULATOR OF NF-KB
; FILE REFERENCE: 0660-0146-55
; CURRENT APPLICATION NUMBER: US/10/408,305
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US/09/253,701
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1874
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-408-305-2

Alignment Scores:
Pred. No.: 2,26e-147 Length: 1874
Score: 1822.50 Matches: 362
Percent Similarity: 90.93% Conservative: 19
Best Local Similarity: 86.40% Mismatches: 31
Query Match: 86.17% Indels: 7
DB: 17 Gaps: 1

US-09-377-795-2 (1-419) x US-10-408-305-2 (1-1874)

QY 1 MetAsnArgHisLeuTyrLysSerGlnLeuGluMetValGlnProSerGlyGlyPro 20
Db 94 ATGAACACGACCCCTCGAAGAACACAGCTGAGTGAGACGGTGCGACCCAGTGGTGGCCCA 153

QY 21 AlaAlaAspGlnAspValLeuGluGlyGluSerProLeuGluGlySerProAlaMetLeuHis 40
Db 154 GCAGAGACACGAGCATGCTGGGTGAGAAATCTTCTCGGGAAGCCTCAATGCTACAT 213

QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluAsnGlnGlu 60
Db 214 CTGCCTTCAGACGAGGCTACTCTCGAGACCTCCAGCGCTGCTGAGAGAAATCAAGAG 273

QY 61 LeuArgAspAlaLeuArgGlnSerAsnGlnLeuLeuArgGluArgCysGluLeuLeu 80
Db 274 CTCGAGACGCTATCCGGCAGAGCAATCAGATGCTGAGGGAACGCTGTGAGGAGCTGCTG 333

QY 81 HisPheGlnAlaSerGlnArgGluGluGlyGluPheLeuMetCysLysPheGlnGluAla 100
Db 334 CATTTCCAGCTCAGCCAGCGGAGGAGAGAGTTCCTTATGTGCAATTCAGGAAGCC 393

QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
Db 394 CGGAAGCTGTGGAGAGACTGAGCTTGGAGAAGCTTGATCTTCGGAGTCAGAGGGAACAG 453

QY 121 AlaLeuArgValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140
Db 454 GCCTTAAGAGGTGGAGCACTGGAAGAAATGCCAACAGCAGATGCTGAGGACAAGGCC 513

QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGluSerGlnSerArgLeu 160
Db 514 TCTGTGAAGCTCAGGTGACATCATTTGCTCGAGAACTCCAGAGAGCCAGACGCGTTG 573

QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
Db 574 GAGCTGCCACCAAGATCGGAAGCTTTAGAGGAAGGATTCGAGCAGATTAGTGAGCAG 633

QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
Db 634 GTCAGACAGCTGGAGAGTGGCGGAGGTGCTACAGCAGCAGCAGCAGCTCAGGTGAC 693

QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaLeuArgMetGluArgGlnAlaAla 220
Db 694 CAGCTCGTATGCAGAACACAGAGCGTGGAGGTGCTGCTTCCGAATGGAGCGGAGCTGCT 753

QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnPheGlnGlu 240
Db 1 ATGAGCTGGAAGATCTCAACAGCAGCTCCAGAGGCGGAGGAGGCGCTGGTGGCCAAA 60
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Db 754 TCAGAGGAGAAGCGGAAGCTGGCTCAGTTGCAGGAGCGCCTATCACCAACTCTTCCAAGAC 813
QY 241 TyrAspAsnHisIleLysSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
Db 814 TAGCAGACCCACATTAAGAGCAGC-----AAGGCGATGCAAGCTG 852
QY 261 GluAspLeuLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280
Db 853 GAAGATCTGAGGCAACAGCTCCAGCAAGCTGAGGAGGCCCTGTTAGTGGAGAAATG 912
QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300
Db 913 ATTGATAAGCTGAAAGAGAGGAGCTGAGCAGCAACAAGATTGTGATGAGACTGTGCCAGTC 972
QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
Db 973 TTGAAGGCCCGAGCGGATATCTCAAGGCTGACTTCCAGGCTGAGAGGATGCCCGGAG 1032
QY 321 LysLeuAlaGluLysLysGluLeuGlnGlnGlnLeuGlnGlnArgGluTyr 340
Db 1033 AAGCTGTGTGAGAAAGAGAGTATTTGAGGAGCAGCTGAGCAGCTGCGAGCTTC 1092
QY 341 SerLysLeuLysAlaSerCysGlnGluSerAlaArgIleGluAspMetArgLysArgHis 360
Db 1093 AACAAAGCTGAAAGTGGCTGCATGATGACCGAGATTGAGGATATGAGGAAGCGGCAT 1152
QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerProLeuAla 380
Db 1153 GTAGAGACTCCCGAGCCTCTTTACTCCTGCTCCAGCTCACCCTCTCTTTCATTTGGCC 1212
QY 381 LeuProSerGlnArgArgSerProProGluGluProProAspPheCysCysProLysCys 400
Db 1213 TTGTCCACCAAGCGGAGGAGCCCTCCAGAAACCTCCTGACTTCTGTGTGTCGAGTGC 1272
QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
Db 1273 CAGTATCAGGCTCTGTATATGGACACTCTACAGATACATGTCTATGGAGTGCATAGAG 1329

RESULT 12
US-10-792-063-8
; Sequence 8, Application US/10792063
; Publication No. US20040175797A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jason
; APPLICANT: Garrett-Engle, Phillip
; APPLICANT: Kan, Zhengyan
; TITLE OF INVENTION: IKKKG
; FILE REFERENCE: R03-011-208PV
; CURRENT APPLICATION NUMBER: US/10/792,063
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 06/452,293
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-792-063-8

Alignment Scores:
Pred. No.: 2,33e-62 Length: 486
Score: 827.00 Matches: 162
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 39.10% Indels: 0
DB: 18 Gaps: 0

US-09-377-795-2 (1-419) x US-10-792-063-8 (1-486)

QY 258 MetGlnLeuGluAspLeuLysGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLys 277
Db 1 ATGAGCTGGAAGATCTCAACAGCAGCTCCAGAGGCGGAGGAGGCGCTGGTGGCCAAA 60
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QY 278 GlnGluValIleAspLysLeuLysGluAlaGluGlnHisLysIleValMetGluThr 297  
DB 61 CAGGAGTGATCGATAGCTGAAGGAGAGCCGAGGAGCACAAGATTGTGATGGAGACC 120  
QY 298 ValProValLeuLysAlaGlnAlaAspIleTyrlsAlaAspPheGlnAlaGluArgGln 317  
DB 121 GTTCCGGTGTGAAGGCCAGGCCGATATCTACAAGGCGGACTTCCAGGCTGAGAGGCAG 180  
QY 318 AlaArgGluLysLeuAlaGluLysLysGluLeuLeuGlnGlnLeuGlnLeuGln 337  
DB 181 GCCCGGAGAGCTGGCCGAGAGAGAGGCTCTCGAGGAGCAGCTGGAGCAGCTGCAG 240  
QY 338 ArgGluTyrlsLysLeuLysAlaSerCysGlnGluSerAlaArgIleGluAspMetArg 357  
DB 241 AGGAGGTACAGCAAACTGAAGGCCAGCTGTGAGAGTGGCCAGGATCGAGGACATGAGG 300  
QY 358 LysArgHisValGluValSerGlnAlaProLeuProProAlaProAlaTyrlsLeuSerSer 377  
DB 301 AAGCGGCATGTCGAGGTCTCCAGGCCCTTGGCCGCCCTTGGCCCTTACCTTCTCTCT 360  
QY 378 ProLeuAlaLeuProSerGlnArgSerProGluGluProProAspPheCysCys 397  
DB 361 CCCTGGCCCTGGCCAGCAG 420  
QY 398 ProLysCysGlnTyrlsGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCys 417  
DB 421 CCCAAGTGCAGTATCAGGCCCTTGATATGACACACCTCGACATACATGTCATGGAGTGC 480  
QY 418 IleGlu 419  
DB 481 ATTGAG 486

## RESULT 13

US-10-792-063-6

; Sequence 6, Application US/10792063

; Publication No. US20040175797A1

; GENERAL INFORMATION:

; APPLICANT: Johnson, Jason

; APPLICANT: Garrett-Engle, Phillip

; APPLICANT: Kan, Zhengyan

; TITLE OF INVENTION: IKRG

; FILE REFERENCE: R03-011-208PV

; CURRENT APPLICATION NUMBER: US/10/792,063

; CURRENT FILING DATE: 2004-03-03

; PRIOR FILING DATE: 2004-03-03

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 6

; LENGTH: 483

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-792-063-6

## Alignment Scores:

Pred. No.:	2,72e-56	Length:	483
Score:	756.50	Matches:	159
Percent Similarity:	63.49%	Conservative:	1
Best Local Similarity:	63.10%	Mismatches:	0
Query Match:	35.77%	Indels:	92
DB:	18	Gaps:	1

US-09-377-795-2 (1-419) x US-10-792-063-6 (1-483)

QY 1 MetAspArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
DB 1 ATGAATAGGCACCTCTGGAAGAGCCAACTGTGTGAGATGTCGAGCCAGCCAGTGGTGGCCCG 60  
QY 21 AlaAlaAspGlnAspValLeuGluGluSerProLeuGlyLysProAlaMetLeuHis 40  
DB 61 GCAGCAGATCAGGACGATCTGGGCGAAGAGTCTCTCTGTCGGGAAGCCAGCCATGCTGCAC 120

QY 41 LeuProSerGluGlnGlnAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60  
DB 121 CTGCTTTAGAACAGAGGCGCTCTTGAGACCTCTCAGCGCTGCTTGGAGGAGATCAAGAG 180  
QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluLeuLeu 80  
DB 181 CTCCGAGATGCCATCCGGCAGAGCAACAGATTCTGCGGAGCGCTCGCAGGAGCTTCTG 240  
QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100  
DB 241 CATTTCCAGCCAGCCAGAGGAGGAGAGAGTTCCTCATGTGCAAGTTTCCAGGAGGCC 300  
QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnGluGln 120  
DB 301 AGAAACTGGTGGAGAGACTCGGCCCTGGAGAGCTCGATCTGAAGAGGCAAGAGGACAG 360  
QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140  
DB 361 GCTCTCGGAGGAGTGGAGCACCTGAAGAGATGCCAG----- 396  
QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerArgLeu 160  
DB 396 ----- 396  
QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaAlaArgAlaAlaSerGluGln 180  
DB 396 ----- 396  
QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200  
DB 396 ----- 396  
QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220  
DB 396 ----- 396  
QY 221 SerGluGluLys-ArgLysLeuAlaGlnLeuGlnValAlaTyrlsHisGlnLeuPheGlnGln 240  
DB 397 -----CAGGAGGAGAGCTGGCCAGCTTGAGGTGGCTATCACCAGCTCTTCCAGA 447  
QY 240 uTyrlsAspAsnHisIleLysSerSerValValGly 251  
DB 448 ATACGACCAACCATCATCAGAGCAGCGCTGGTGGGC 481

RESULT 14  
US-09-863-049A-1  
; Sequence 1, Application US/09863049A  
; Publication No. US20030032055A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenrick, Sue J.  
; APPLICANT: Nelson, David L.  
; APPLICANT: Aradhya, Swaroop  
; APPLICANT: D'Urso, Michele  
; APPLICANT: Woffendin, Hayley  
; APPLICANT: Munnich, Arnold  
; APPLICANT: Smahi, Asmaa  
; APPLICANT: Israeli, Alain  
; APPLICANT: Poustka, Annemarie  
; APPLICANT: Lewis, Richard A  
; APPLICANT: Levy, Moise  
; APPLICANT: Heiss, Nina  
; TITLE OF INVENTION: Diagnosis and Treatment of Medical Conditions Associated with Defect  
; FILE REFERENCE: HO-P01961US1  
; CURRENT APPLICATION NUMBER: US/09/863,049A  
; CURRENT FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/206,223  
; PRIOR FILING DATE: 2000-05-22  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 23106  
; TYPE: DNA



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Db 20121 CACCTCTGACCAGGTGGCAGAGTGAAGGACTGAGGGCTCTCAGCTGAGCTGTGCACATG 20180
QY 256 -----
Db 20181 GCGGGCACAGACCGGCTGGCTGTGTAGTGGGTGTGGCTGTGGCTGTGAAGGTGGAG 20240
QY 256 -----
Db 20241 GAGGCTGTGAGCTGGGATTCTGGGAGGGAATGTGGCCAGCTGGGAGGTGTATCC 20300
QY 256 -----
Db 20301 AGATGACCTCAGCGGCTCTTCAGTCTCTGAAAAAACCCTCAGCATCTCCTCTGTCGTTTT 20360
QY 256 -----
Db 20361 GGGCGGTGACAGGACGAGCCATCTCCCTGTGACGTGAGATCCTGCAATGGGCCCTCA 20420
QY 256 -----
Db 20421 AATCAGGGGTGGCATCACCCAGCCTGGTCAGCGGGCCACTCTTTTCATCCTTCTCAGT 20480
QY 256 -----
Db 20481 TCTTCTCAGCCAGCCTCGCCCTGGGCTGACGAGGCTCCGTGAGCTCCCTTTGCCCGTCT 20540
QY 257 ---GlyMetGlnLeuGluAspLeuLysGlnGlnLeuGlnAlaGluAlaLeuVal 275
Db 20541 TAGGGAAATGACGTGGGAAGATCTCAACAGCAGCTCCAGCAGGCGCGAGGCGCTGGT 20600
QY 276 AlalysGlnGluValIleAspLysLeuLysGluAlaGluGlnHisLysIleValMet 295
Db 20601 GCCAAACAGAGGTGATCGATAGCTGAGAGAGGCCGAGCAGCAAGATTGTGATG 20660
QY 296 GluThrValProValLeuLysAla----- 303
Db 20661 GAGACCGTTCGGTGTGAAGGCCAGGTGAGGGCCCTCTCTCTGACCCACCCTGGCAC 20720
QY 303 -----
Db 20721 TGGGACCTGAGAGTCTCTTTGGCGTCTTTTTTTTTTTTTTTTTTTTGTCTTTTGTAGA 20780
QY 303 -----
Db 20781 TTGAGTTTTGCTCTTGTGGCCAGGCTGGAGTGCCTAGTGGCAGCATCTTGGCTCACT 20840
QY 303 -----
Db 20841 GCAACCTCTGCCTTCGGGTTCAAAACAATTCTCTTTGCCTCAGCCTCCTGAGTAGTGG 20900
QY 303 -----
Db 20901 ATTACAGGCGCTGCGCCATGCCGCTAAATTTTGTATTTTATTTAGTAGACAGGGTTT 20960
QY 303 -----
Db 20961 CACCATGTTGGCCAGCTGCTCGAACTTCTGGCCTCAGGTGATCTGCCACCGCAGTC 21020
QY 303 -----
Db 21021 TCTCAAAAGTTCTGGGATTACAGGCGTGAGCCACCGCACCGGCTCTTTGGCATCATTTT 21080
QY 303 -----
Db 21081 GTAGTGGCCTTTCTGATAGCTTCTGAGCCTGTTGTGCTCTCTTAGACCTCTCGGTGAGC 21140
QY 303 -----
Db 21141 TTGGCATTAATCGCCGACGATCTGTTTCTCTGACCCGCTGGGGCTCTGGGAGGACAG 21200
QY 303 -----
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Db 21201 CAGTGGGTTCTGCTTTTGTCTGTGTGCTGGCAGTGCCTGGTGGTGGCTGGCTTG 21260
QY 304 -----GlnAlaAspIleTyrLysAlaAspPheG 313
Db 21261 TGGCGGGCACATCCCTTTCTGTGTGGATTTTCCAGCGGATATCTTACAAGCGGACTTTCCA 21320
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Db 21321 GGCTGAGGACAGCCCGGAGAGAGCTGGCCGAGAGAGAGCTCTTCAGGAGCAGCT 21380
QY 333 uGluGlnLeuGlnAArgGluTyrSerLysLeuLysAlaSerCysGlnGluSerAla----- 351
Db 21381 GGAGCAGCTGACAGGAGGTACAGCAAACTGAAGGCCAGCTGTCCAGGAGTCGGC- CAGGT 21439
QY 351 -----
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QY 371 -----
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QY 371 -----
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QY 371 -----
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QY 371 -----
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QY 372 -----ProAlaTyrLeuSerSerProLeuAlaLeuProSerGlnAArgSerP 388
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QY 388 roProGluProProAspPheCysCysProLysCysGlnTyrGlnAlaProAspMetA 408
Db 22100 CCCCCGAGGAGCCACCTGACTTCTGTCTGCCAAGTGCCAGTATCAGGCCCTGATATGG 22159
QY 408 spThrLeuGlnIleHisValMetGluCysIleGlu 419
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## RESULT 15

US-09-925-298-84/c  
; Sequence 84, Application US/09925298  
; Publication No. US20020039764A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

Thu Feb 10 11:03:43 2005

FILE REFERENCE: PA103  
CURRENT APPLICATION NUMBER: US/09/925,298  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05881  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 846  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 84  
LENGTH: 2803  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (10)  
OTHER INFORMATION: n equals a,t,g, or c  
NAME/KEY: misc feature  
LOCATION: (50)  
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NAME/KEY: misc feature  
LOCATION: (1926)  
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US-09-925-298-84

Alignment Scores:  
Pred. No.: 2,14e-28 Length: 2803  
Score: 443.00 Matches: 85  
Percent Similarity: 94.51% Conservative: 1  
Best Local Similarity: 93.41% Mismatches: 5  
Query Match: 20.95% Indels: 0  
DB: 9 Gaps: 0

US-09-377-795-2 (1-419) x US-09-925-298-84 (1-2803)

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Qy	21	AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis	40
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Qy	41	LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluAsnGlnGlu	60
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Qy	61	LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu	80
Db	104	CTCGAGATGCCATCCGGCAGACCAACAGATTTTTCGGGACCTTGGCARGAGNTTTTG	45
Qy	81	HisPheGlnAlaSerGlnArgGluGluLysGlu	91
Db	44	SATTTCCAGCCAGCCAGAGGAGGAGGAGGAT	12

Search completed: February 9, 2005, 06:53:53  
Job time : 1660 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 9, 2005, 01:01:13 ; Search time 5944 Seconds  
(without alignments)  
3415.669 Million cell updates/sec

Title: US-09-377-795-2

Perfect score: 2115

Sequence: 1 MNRHLKSQLCENVPVSGGP.....COYQAPDMDTLQIHVMECIE 419

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO\_spool/US03377795/runat\_07022005\_112551\_12117/app\_query.fasta\_1.583  
-DB=genembl -QFWT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
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-USER=US03377795 @CGN 1 1 4200 @runat\_07022005\_112551\_12117 -NCPU=6 -ICPU=3  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*

1: gb\_ba.\*  
2: gb\_hgt.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2115	100.0	1966	9 BC000299	Homo sapi
2	2115	100.0	1990	9 BC050612	Homo sapi
3	2115	100.0	1994	9 AF074382	Homo sapi
4	2115	100.0	2009	6 BD135431	Receptor

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	2115	100.0	2009	6	CQ867779	Sequence
6	2115	100.0	2009	6	AR534835	Sequence
7	2115	100.0	2009	6	AX017214	Sequence
8	2115	100.0	2035	9	AF091453	Homo sapi
9	2115	100.0	2071	9	BC012114	Homo sapi
10	2115	100.0	2073	9	AY114157	Homo sapi
11	2115	100.0	2121	9	AF261086	Homo sapi
12	2105	99.5	1975	9	AF062089	Homo sapi
13	2028.5	95.9	2034	6	BD135432	Receptor
14	2028.5	95.9	2034	6	CQ867780	Sequence
15	2028.5	95.9	2034	6	AR534836	Sequence
16	2028.5	95.9	2034	6	AX017215	Sequence
17	1848.5	87.4	1239	10	AY392762	Rattus no
18	1828.5	86.5	1798	10	AF513109	Mus muscu
19	1828.5	86.5	2250	10	AY112937	Mus muscu
20	1822.5	86.2	1748	10	AF069542	Mus muscu
21	1822.5	86.2	1874	6	AR454143	Sequence
22	1813	85.7	2282	10	BC021431	Mus muscu
23	1799	85.1	2175	4	BTA414557	Bos tauru
24	1576.5	74.5	1666	9	AK000593	Homo sapi
25	1414	66.9	2038	6	AX781112	Sequence
26	1149.5	54.3	716	9	AY429546	Homo sapi
27	922.5	43.6	600	9	AY429547	Homo sapi
28	601	28.4	137217	2	HSA211110	Homo sapi
29	594	28.1	202213	2	AC148902	Otolemur
30	589.5	27.9	148309	2	AC146529	Macaca mu
31	589.5	27.9	178507	2	AC146312	Macaca mu
32	589	27.8	136551	2	AC149258	Papio anu
33	589	27.8	165013	2	AC149865	Papio anu
34	584.5	27.6	23106	9	HSA271718	Homo sapi
35	579.5	27.4	126566	9	AC144385	Homo sapi
36	579.5	27.4	155221	2	AC145688	Pan trogl
37	576	27.2	142017	2	HSA196818	Homo sapi
38	551	26.1	147234	9	AF277315	Homo sapi
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40	551	26.1	160656	2	AL592072	Homo sapi
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42	476.5	22.5	2536	5	BC063986	Danio rer
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44	453.5	21.4	188873	2	AC073658	Mus muscu
45	453.5	21.4	198426	10	AC091474	Mus muscu

ALIGNMENTS

RESULT 1	BC000299	1966 bp	mRNA	linear	PRI 04-OCT-2003
LOCUS	Homo sapiens inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma, mRNA (CDNA clone MGC:8374 IMAGE:2820134), complete cds.				
DEFINITION	BC000299				
ACCESSION	BC000299	GI:33875269			
VERSION	BC000299.2				
KEYWORDS	MGC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 1966)				
	Klausner, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.P., Bhat, N.K., Hopkins, R.F., Jordan, K., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,				

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 22388257  
 12477932  
 2 (bases 1 to 1966)  
 Strausberg, R.  
 Direct Submission  
 Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 On Aug 19, 2003 this sequence version replaced gi:12653066.  
 Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: DCTD/DTP  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)  
 Gaithersburg, Maryland  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: [nisc\\_mgc@nri.nih.gov](mailto:nisc_mgc@nri.nih.gov)  
 Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Green, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 1 Row: c Column: 5  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21361093.

## FEATURES

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## gene

## CDS

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 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0  
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 QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
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 QY 261 GluAspLeuLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuAlaLysGlnGluVal 280  
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QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
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LOCUS Homo sapiens Ikb kinase gamma subunit (IKK-gamma) mRNA, complete
DEFINITION cds.
ACCESSION AF074382
VERSION AF074382.1 GI:3641279
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 (bases 1 to 1994)
AUTHORS Rothwarf,D.M., Zandi,E., Natoli,G. and Karin,M.
TITLE IKK-gamma is an essential regulatory subunit of the IkappaB kinase complex
JOURNAL Nature 395 (6699), 297-300 (1998)
MEDLINE 98421680
PUBMED 9751060
REFERENCE 2 (bases 1 to 1994)
AUTHORS Rothwarf,D.M., Zandi,E., Natoli,G. and Karin,M.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1998) Pharmacology, University of California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0636, USA
FEATURES
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QY	161	GluAlaAlaThrLysGluCysGlnAlaLeuGluGluArgAlaArgAlaAlaSerGluGln	180
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ACCESSION	BD135431					
VERSION	BD135431.1					
KEYWORDS	JP 2002506644-A/1.					
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ORGANISM	Homo sapiens					
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REFERENCE	1 (bases 1 to 2009)					
AUTHORS	Wallach,D., Kovalenko,A., Horwitz,M.S. and Li,Y.					
TITLE	Receptor function regulator for TNF/NGF receptor family and other proteins					
JOURNAL	Patent: JP 2002506644-A 1 05-MAR-2002;					
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COMMENT	OS Homo sapiens (human)					
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	PF 18-MAR-1999 JP 2000536855					
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	CC Receptor function regulator for TNF/NGF receptor family and other proteins					
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VERSION CQ867779.1 GI:51997898
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SOURCE Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Wallach,D. and Kovalenko,A.
TITLE Modulators of receptors of the tnfr/ngf receptor family
JOURNAL Patent: EP 1454985-A 1 08-SEP-2004;
FEATURES YEDA RESEARCH & DEVELOPMENT COMPANY, LTD. (IL)
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ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 2009)
AUTHORS   Wallach,D., Kovaleiko,A., Horwitz,M.S. and Li,Y.
TITLE     Modulators of the function of receptors of the TNF/NGF receptor
JOURNAL   Patent: US 6734174-A 1 11-MAY-2004;
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Alignment Scores:
Pred. No.:      4..4e-110      Length:      2009
Score:          2115.00      Matches:      419
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
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Db      214  GCAGCAGATCAGGACGACTGGGGGAAGAGTCTCTCTGGGGGAAGCCAGCATGCTGCAC 273
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ORGANISM Homo sapiens  
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AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.  
JOURNAL Wallach, D., Kovalevko, A., Li, Y. and Horwitz, M.S.  
AUTHORS Modulators of the function of receptors of the tnfr/ngf receptor  
TITLE family and other proteins  
JOURNAL Patent: WO 9947672-A 1 23-SEP-1999;  
AUTHORS WALLACH DAVID (IL); YEDA RES & DEV (IL); KOVALENKO ANDREI (IL);  
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TITLE Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.  
JOURNAL Jin, D.Y. and Jeang, K.T.  
AUTHORS Isolation of full-length cDNA and chromosomal localization of human  
TITLE NF-kappaB modulator NEMO to Xq28  
JOURNAL J. Biomed. Sci. 6 (2), 115-120 (1999)  
MEDLINE 99189402  
PUBMED 10087442  
REFERENCE  
AUTHORS Jin, D.Y., Giordano, V., Kibler, K.V., Nakano, H. and Jeang, K.T.  
TITLE Role of adapter function in oncoprotein-mediated activation of  
NF-kappaB. Human T-cell leukemia virus type I Tax interacts  
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JOURNAL J. Biol. Chem. 274 (25), 17402-17405 (1999)  
MEDLINE 99292691

PUBMED 10364167  
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 AUTHORS Jin, D.Y.  
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 REFERENCE 1 (bases 1 to 2071)  
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
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Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzyzanski, M.I., Skalska, U., Smalhus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences (26), 16899-16903 (2002)

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 2071)

Direct Submission

Submitted (02-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [scapsb@mail.nih.gov](mailto:scapsb@mail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada

[info@bcgsc.bc.ca](mailto:info@bcgsc.bc.ca)

Sueven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzyzanski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21361093.

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AUTHORS Perelygin,A.A. and Perelygina,L.M.
TITLE Ikbk gene modulates the herpes virus susceptibility in mice
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2073)
AUTHORS Perelygin,A.A. and Perelygina,L.M.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2002) Biology, Georgia State University, 24
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 Best Local Similarity: 100.00% Mismatches: 0  
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US-09-377-795-2 (1-419) x AY114157 (1-2073)

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 Ye, Z. and Connor, J.R.  
 cDNA cloning by amplification of circularized first strand cDNAs  
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 Biochem. Biophys. Res. Commun. 275 (1), 223-227 (2000)  
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 Ye, Z. and Connor, J.R.  
 Direct Submission  
 Submitted (27-APR-2000) Neuroscience and Anatomy, Pennsylvania  
 State University College of Medicine, 500 University Drive,  
 Hershey, PA 17033 USA

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## ORIGIN



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REFERENCE 1 (bases 1 to 2034)
AUTHORS Wallach,D., Kovalenko,A., Horwitz,M.S. and Li,Y.
TITLE Receptor function regulator for TNF/NGF receptor family and other
proteins
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ORIGIN

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 Pred. No.: 3,26-105 Length: 2034  
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US-09-377-795-2 (1-419) x AR534836 (1-2034)

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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Perfect score: 2115

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-USER=US09377795 @CGN 1.1 644 @runat\_07022005\_112550\_12108 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 16Dec04:\*

1:	Geneseqn1980s:*
2:	Geneseqn1990s:*
3:	Geneseqn2000s:*
4:	Geneseqn2001as:*
5:	Geneseqn2001bs:*
6:	Geneseqn2002as:*
7:	Geneseqn2002bs:*
8:	Geneseqn2003as:*
9:	Geneseqn2003bs:*
10:	Geneseqn2003cs:*
11:	Geneseqn2003ds:*
12:	Geneseqn2004as:*
13:	Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2115	100.0	1967	13	Adq87415 Human tum
2	2115	100.0	1967	13	Adq86256 Human tum
3	2115	100.0	1994	3	Aac81426 Human i-k
4	2115	100.0	1994	3	Aaa35027 Human ade
5	2115	100.0	1994	3	Aaf21149 Human low

6	2115	100.0	1994	8	ADA44705
7	2115	100.0	1994	10	ABZ96843
8	2115	100.0	1994	10	ABV75393
9	2115	100.0	1994	11	ABD20692
10	2115	100.0	2009	2	AAZ07513
11	2115	100.0	2035	9	ACD23012
12	2115	100.0	8631	3	AAA35028
13	2115	100.0	8631	3	AAF21150
14	2115	100.0	8631	10	ABZ96844
15	2115	100.0	8631	11	ABD20693
16	2105	99.5	1260	12	ADK71964
17	2105	99.5	1975	8	ADA44712
18	2028.5	95.9	2034	2	AAZ07514
19	1840.5	87.0	1104	13	ADS17862
20	1822.5	86.2	1874	12	ADC36537
21	1822.5	86.2	1874	12	ADI61940
22	1822.5	86.2	1874	12	ADI29002
23	1822.5	86.2	1874	13	ADI61943
24	1414	66.9	2038	10	ADF82713
25	827	39.1	486	13	ADS17866
26	756.5	35.8	483	13	ADS17864
27	584.5	27.6	23106	9	ACD23011
28	443	20.9	2803	3	AAF21697
29	436.5	20.6	1925	12	ADO43193
30	436.5	20.6	2076	12	ADO43195
31	430.5	20.4	1752	12	ADP80916
32	430.5	20.4	2023	12	ADO43191
33	420.5	19.9	1734	12	ADL14949
34	420.5	19.9	1856	9	ACF03997
35	420.5	19.9	1856	12	ADO43185
36	420.5	19.9	2008	9	ACF03998
37	420.5	19.9	2008	12	ADO43187
38	420.5	19.9	2077	9	ACF03996
39	420.5	19.9	2077	12	ADO43183
40	420.5	19.9	2108	10	ADL24738
41	420.5	19.9	2139	10	ADL15031
42	420.5	19.9	2139	12	ADP13343
43	420.5	19.9	2139	13	ADR24267
44	420.5	19.9	2327	13	ADR14212
45	420.5	19.9	2327	13	ADP23351

#### ALIGNMENTS

RESULT 1  
ADQ87415  
ID ADQ87415 standard; cDNA; 1967 BP.  
XX  
AC ADQ87415;  
XX  
DT 07-OCT-2004 (first entry)  
XX  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4292.  
XX  
KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;  
XX  
OS Homo sapiens.  
XX  
PN WO2004060270-A2.  
XX  
PD 22-JUL-2004.  
XX  
PF 15-OCT-2003; 2003WO-US029126.  
XX  
PR 18-OCT-2002; 2002US-0418988P.  
XX  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
PI Wu TD, Zhou Y;  
XX



AC	ADQ86256;	Alignment Scores:	
XX	07-OCT-2004 (first entry)	Pred. No.: 8,666-153	Length: 1967
DE	Human tumour-associated antigenic target (TAT) cDNA sequence #3128.	Score: 2115.00	Matches: 419
XX	human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;	Percent Similarity: 100.00%	Conservative: 0
KW	cancer; cell proliferative disorder; gene; ss.	Best Local Similarity: 100.00%	Mismatches: 0
XX	Homo sapiens.	Query Match: 100.00%	Indels: 0
XX		DB: 13	Gaps: 0
XX	WO2004060270-A2.	US-09-377-795-2 (1-419) x ADQ86256 (1-1967)	
XX	22-JUL-2004.		
XX	15-OCT-2003; 2003WO-US029126.		
XX	18-OCT-2002; 2002US-0418988P.		
XX	(GETH ) GENENTECH INC.		
PA	(WUTD/) WU T D.		
PA	(ZHOU/) ZHOU Y.		
XX	Wu TD, Zhou Y;		
PI	WPI; 2004-534300/51.		
DR	New nucleic acid molecule and encoded polypeptide, for diagnosing,		
XX	preventing or treating cell proliferative disorders such as cancer.		
XX	Claim 1; SEQ ID NO 3128; 5504pp; English.		
CC	The present invention describes an isolated tumour-associated antigenic		
CC	target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide		
CC	sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of		
CC	(a); (c) the complement of (a) or (b); (d) a sequence that has 80%		
CC	sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-		
CC	(c). Also described: (1) an expression vector comprising the above		
CC	nucleic acid; (2) a host cell comprising the above expression vector; (3)		
CC	a process for producing a polypeptide; (4) an isolated polypeptide		
CC	comprising: (a) an amino acid sequence encoded by any of the above		
CC	nucleotide sequences; (b) an amino acid sequence encoded by the full-		
CC	length coding region of the above nucleotide sequences; or (c) a sequence		
CC	having at least 80% identical to (a) or (b); (5) a chimeric polypeptide		
CC	comprising the above polypeptide fused to a heterologous polypeptide; (6)		
CC	an isolated antibody that binds to the above polypeptide; (7) a process		
CC	for producing the antibody; (8) an isolated oligopeptide that binds to		
CC	the above polypeptide; (9) a tumour-associated antigenic target (TAT)		
CC	binding organic molecule that binds to the above polypeptide; (10) a		
CC	composition of matter comprising the above (chimeric) polypeptide,		
CC	antibody, oligopeptide or TAT binding organic molecule, in combination		
CC	with a carrier; (11) an article of manufacture comprising a container and		
CC	the composition of matter contained within the container; (12) methods of		
CC	inhibiting the growth of a cell that expresses the above protein, where		
CC	the growth of the cell is at least in part dependent upon a growth		
CC	potentiating effect of the above protein; (13) a method of		
CC	therapeutically treating a mammal having a cancerous tumour comprising		
CC	cells that express the above protein; (14) a method of determining the		
CC	presence of a protein in a sample suspected of containing the protein		
CC	described above; (15) methods of diagnosing the presence of a tumour in a		
CC	mammal; (16) a method for treating or preventing a cell proliferative		
CC	disorder associated with increased expression or activity of the above		
CC	protein; and (17) a method of binding an antibody, oligopeptide or		
CC	organic molecule to a cell that expresses the protein described above.		
CC	The TAT sequences have cytostatic activities, and can be used in gene		
CC	therapy. The composition and methods are useful for diagnosing,		
CC	preventing or treating cancer. The composition is also used for preparing		
CC	a medicament for the therapeutic treatment or diagnostic detection of a		
CC	cell proliferative disorder or cancer. The present sequence represents a		
CC	human TAT cDNA sequence from the present invention.		
XX	Sequence 1967 BP; 409 A; 581 C; 629 G; 348 T; 0 U; 0 Other;		
SO			



341 SerLysLeuLysAlaSerCysGlnGluSerAlaArgIleGluAspMetArgLysArgHis 360  
 1169 AGCAAACTGAAGCCACCTGTCTAGGAGTGGCCAGGATCGAGACATGAGAGCGGCAT 1228  
 361 ValGluValSerGlnAlaProLeuProProAlaProAlaProAlaProAlaProLeuAla 380  
 1229 GTGAGGTCTCCAGGCGCCCTTGGCCCGCCCTTACCTCTCTCCCTGGCC 1288  
 381 LeuProSerGlnArgArgSerProProGluGluProProAspPheCysCysProLysCys 400  
 1289 CTGCCAGCCAGAGGAGGAGCCCGCCGAGGAGCCCTGACTTCTGCTCCCAAGTGC 1348  
 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419  
 1349 CAGTATCAGGCCCTGATATGGACACCTCGACATACATCTCATGGATGTCATTGAG 1405

RESULT 4  
 AAA35027  
 ID AAA35027 standard; DNA; 1994 BP.  
 XX  
 AC AAA35027;  
 XX  
 XX 28-JUL-2000 (first entry)  
 DT  
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2716.  
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphothioate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antasthmatic; cyostatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200009525-A2.  
 PN  
 XX 24-FEB-2000.  
 PD  
 XX 03-AUG-1999; 99WO-US017712.  
 PF  
 XX 03-AUG-1998; 98US-0095212P.  
 PR  
 XX (UYEC-) UNIV EAST CAROLINA.  
 PA  
 XX Nyce JW;  
 PI  
 XX WPI; 2000-205971/18.  
 DR  
 XX New antisense oligonucleotides useful for treating e.g. pulmonary  
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 PT cancers.  
 XX  
 PS Disclosure; Page 968-969; 1343pp; English.  
 XX  
 CC The present invention describes a new composition comprising an antisense  
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
 CC nucleic acids involved in bronchoconstriction, allergies, and/or  
 CC inflammation. The ON can have antiinflammatory, antiallergic,  
 CC antisthmatic, cyostatic and analgesic activities. The compositions are  
 CC useful for the treatment of diseases associated with inflammation,  
 CC impaired airways, including lung disease and diseases whose secondary  
 CC effects afflict the lungs of a subject. They can be used for treating  
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
 CC impeded respiration, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
 CC carcinomas, and cancers which may metastasise to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of the  
 CC ONs reduces side effects. The A-containing ONs break down with the

CC release of deoxyadenosine which activates adenosine receptors causing  
 CC bronchoconstriction and inflammation. AAA32313 to AAA3512 represent the  
 CC nucleotide sequences given in the sequence listing from the present  
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
 CC Sequences given in the disclosure of the present invention do not match  
 CC up with their corresponding SEQ ID NO: sequences given in the sequence  
 CC listing  
 XX  
 SQ Sequence 1994 BP; 429 A; 585 C; 633 G; 347 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.8e-153 Length: 1994  
 Score: 2115.00 Matches: 419  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0  
 US-09-377-795-2 (1-419) x AAA35027 (1-1994)  
 QY 1 MetAsnArgHisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
 DB 149 ATGAATAGGCACCTCTGGAAAGAGCCCAACTGTGTGAGATGGTGAGCCCATGGTGGCCG 208  
 QY 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40  
 DB 209 GCAGCAGATCAGGACGTACTTGGGCGAAGAGTCTCTCTGGGGGAAGCAGCAGCATGCTGCAC 268  
 QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAenGlnGlu 60  
 DB 269 CTGCTTTCAGAACAGGGCGCTCTGTAGACCTCTCAGCGCTGCTGAGGAGGAATCAAGAG 328  
 QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80  
 DB 329 CTCGAGATGCCATCCGCGCAGACCAACAGATTCTCGGGAGCGCTGCGAGGAGCTTCTG 388  
 QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100  
 DB 389 CATTTCCAAAGCCAGCCAGAGGGAGGAGAGTCTCTCATGTGCAAGTTCCAGGAGGCC 448  
 QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120  
 DB 449 AGGAAACTGCTGGAGAGACTTCGCGCTGGAGAAAGCTCGATCTGAAGAGGCGAAGAGGACG 508  
 QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140  
 DB 509 GCTCTGCGGGAGGTGGAGCACCTGAAAGAGATGCCAGCAGCAGATGCTGAGGACAGGCC 568  
 QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160  
 DB 569 TCTGTAAAGCCCGAGTGCCTCTTGTCTCGGGAGCTGCGAGGAGCAGCAGAGTCTGCTTG 628  
 QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180  
 DB 629 GAGGCTGCCACCTAAAGAAATGCCAGGCTCTGGAGGGTGGCGCCCGCGCGCAGCAGCAG 688  
 QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200  
 DB 689 GCGCGGCAGCTGGAGAGTGGCGGAGGCGCTGCGAGCAGCAGCAGCAGCTGCGAGTGGAC 748  
 QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220  
 DB 749 CAGCTGCGATGCGAGGCCAGAGCGTGGAGGCGCGCTCCGATGAGGCGCCAGCGCGCC 808  
 QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240  
 DB 809 TCGAGGAGAAAGAGGAGGCTGGCCCAAGTTCAGGTTGGCTTATCACCAGCTCTTCCAGAA 868  
 QY 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260

Db 869 TACGACCAACACATCAAGACGAGCGGTGGTGGCAGTACGCGAGCGAGGATGCGCTG 928  
 Qy 261 GluAspLeuLysGlnGlnLeuGlnGlnAlaGluGlnAlaLeuValAlaLysGlnGluVal 280  
 Db 929 GAAGATCTCAAAACAGCAGCTCCAGCAGGCGCCGAGGAGGCGCTGGTGGCCAAACAGGAGGTG 988  
 Qy 281 IleAspLysLeuLysGlnGlnAlaGlnGlnHisLysIleValMetGluThrValProVal 300  
 Db 989 ATCGATAGCTGAAGGAGGAGGCGGAGCAGCACAAGATTGTGATGAGACCGTTCGGGTG 1048  
 Qy 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320  
 Db 1049 CTGAAGCCCGAGCGGATATCTACAAGCGGACTTCCAGCTGAGAGGCGAGGCCCGGAG 1108  
 Qy 321 LysLeuAlaGlnLysLysGlnLeuLysGlnGlnGlnLeuGlnGlnLeuGlnArgGluTyr 340  
 Db 1109 AAGCTGGCCGAGAGGAGGAGCTCTCCAGGAGCAGCTGGAGCAGCTGGAGGAGGTAC 1168  
 Qy 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaAspGlnLeuAspMetArgLysArgHis 360  
 Db 1169 AGCAACTGAAGCCAGCTGTCCAGGAGTCCGCGAGGATCGAGGATGAGGAGCGGAT 1228  
 Qy 361 ValGluValSerGlnAlaProLeuProAlaProAlaProAlaTyrLeuSerSerProLeuAla 380  
 Db 1229 GTGAGGTCTCCAGGCGCCCTTGGCCCGCCCTGCTACCTCTCTCTCTCTCTCTGCCC 1288  
 Qy 381 LeuProSerGlnArgSerProProGluGluProProAspPheCysCysProLysCys 400  
 Db 1289 CTGCCAGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1348  
 Qy 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnGlnIleHisValMetGluCysIleGlu 419  
 Db 1349 CAGTATCAGGCCCTGTATATGGACACCTTCGAGATACATGTCATGAGTGCAATTGAG 1405  
 RESULT 5  
 AAF21149  
 ID AAF21149 standard; DNA; 1994 BP.  
 AC AAF21149;  
 XX  
 XX  
 DT 14-MAR-2001 (first entry)  
 XX  
 DE Human low adenosine antisense oligonucleotide related sequence #2716.  
 XX  
 XX  
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cyostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX W0200062736-A2.  
 XX  
 XX  
 PD 26-OCT-2000.  
 XX  
 XX 24-MAR-2000; 2000WO-US008020.  
 XX  
 XX 06-APR-1999; 99US-0127958P.  
 XX  
 XX (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.  
 XX  
 XX Nyce JW;  
 XX  
 XX WPI; 2000-679539/66.  
 XX  
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger

adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.

Disclosure; Page 1045-1046; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention

Sequence 1994 BP; 429 A; 585 C; 633 G; 347 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 8.8e-153 Length: 1994  
 Score: 2115.00 Matches: 419  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

US-09-377-795-2 (1-419) x AAF21149 (1-1994)

Qy 1 MetAsnArgHisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
 Db 149 ATGAATAGGCACCTCTGGAAGAGCAACTGTGTAGATGGTGCAGCCAGTGGTGGCCCG 208  
 Qy 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40  
 Db 209 GCAGCAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGGAAGCCAGCCATGCTGCAC 268  
 Qy 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnCysLeuGluGluAsnGlnGlu 50  
 Db 269 CTGCCTTCAGAACAGAGGCGCTCTCTGAGACCCCTCCAGGCGCTCGTGGAGAGAGTCAAGAG 328  
 Qy 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80  
 Db 329 CTCGAGATGCCATCCGCGCAGAGCAACAGATCTTCGGGAGCGCTCGAGAGAGCTTCG 388  
 Qy 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100  
 Db 389 CATTTCCAAAGCCAGCCAGGAGGAGAGGAGTTCCTCATGTGCAAGTTCAGAGAGGCC 448  
 Qy 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120  
 Db 449 AGGAAGCTGGTGGAGAGACTCGGCTGGAGAGAGCTCGATCTGAAGAGGAGGAGGAGGAG 508  
 Qy 121 AlaLeuArgGluValGluHisLeuLysLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140





Db 449 AGGAACTGGTGGAGAGACTCGGCTGGAGAGCTGATCTGAAGAGGCGAGAGGAGCG 508  
Qy 121 AlalaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140  
Db 509 GCTTCGGGGAGGTGGAGCACCTGAAGAGATGCGAGAGAGAGAGAGAGAGAGAGAG 568  
Qy 141 SerValLysAlaGlnValThrSerLeuLeuGluGluLeuGlnSerGlnSerArgLeu 160  
Db 569 TCTGTGAAGCCAGGAGTGGAGTCTTGTCTGGGAGCTGAGAGAGAGAGAGAGAGAG 628  
Qy 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGluArgAlaAlaSerGluGln 180  
Db 629 GAGGCTGCCACTAAGGAATCCAGGCTCTGGAGGTCGGGCCCGGCCAGGAGAGAG 688  
Qy 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200  
Db 689 GCGCGGAGGTGGAGAGTGGAGCGAGGCGGCTGAGAGAGAGAGAGAGAGAGAGAG 748  
Qy 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAla 220  
Db 749 CAGTGGCATGAGGCGCCAGAGCGGTGGAGCGCGCTCCGATGGAGCGCCAGCGCC 808  
Qy 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGln 240  
Db 809 TCGAGGAGAGAGAGAGAGCTGGCCAGTTCAGGTGGCTATCACCAGCTCTTCCAGAA 868  
Qy 241 TyrAspHisHisLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260  
Db 869 TAGCACAAACACATCAAGAGAGCGGTGGGCGAGTGGAGCGAGCGAGAGAGAGAG 928  
Qy 261 GluAspLeuLysGlnGlnLeuGlnAlaGluGluAlaLeuValAlaLysGlnVal 280  
Db 929 GAAGATCTCAACAGAGCTTCAGAGCGCGAGAGGCTGCTGGCCAAACAGAGAGTG 988  
Qy 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300  
Db .989 ATCGATAAGCTGAAGAGAGGCGGAGCGAGCACAGATTGTGATGGAGACCGTTC 1048  
Qy 301 LeuLysAlaGlnAlaAspLysLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320  
Db 1049 CTGAAGCCCGAGCGGATATCTACAAAGCGGACTTCCAGGCTGAGAGAGAGCGGAG 1108  
Qy 321 LysLeuAlaGluLysLysGluLeuLeuGlnGlnGlnLeuGlnArgGluTyr 340  
Db 1109 AAGTGGCCGAGAGAGAGAGCTCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGTAC 1168  
Qy 341 SerLysLeuLysAlaSerCysGlnGluSerAlaArgLleGluAspMetArgLysArgHis 360  
Db 1169 AGCAAACTGAAGCCAGCTGTGAGGAGTCCGCGAGATCGAGGACATGAGGAAGCGCAT 1228  
Qy 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380  
Db 1229 GTGAGGTCTCCAGGCGCCCTTGGCCCGCCGCTGCTCTCTCTCTCTCTCTCTCT 1288  
Qy 381 LeuProSerGlnArgSerProGluGluProProAspPheCysCysProLysCys 400  
Db 1289 CTGCCCCAGGAG 1348  
Qy 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419  
Db 1349 CAGTATCAGGCGCCCTGATATGGACACCTCTGAGATACATGTCTATGGATGATGAG 1405

## RESULT 7

ABZ96843  
ID ABZ96843 standard; DNA; 1994 BP.  
XX  
AC ABZ96843;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human nucleic acid sequence.  
XX

Qy 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
Db 149 ATGAATAGGCACCTCTGGAAGAGCAACTGTGTGAGATGTTGTCAGCCAGTGGTGGCCG 208  
Qy 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40  
Db 209 GCAGCAGATCAGGACGTACTGGGCGAAGAGTCTCTCTTGGGGAAGCCAGCCATGCTGCAC 268  
Qy 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60

Human; antisense; lung dysfunction; nasal airway dysfunction;  
antifungal steroid; ubiquinone; anti-inflammatory; anti-allergic;  
antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
antisense gene therapy; respiratory; lung; adenosine sensitivity;  
adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
Miller S, Tang L, Shahabuddin S;  
WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired

respiration, has oligo(s) antisense to specific gene(s) or its  
corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
ubiquinone.

Disclosure; SEQ ID NO 12085; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a  
first active agent comprising an oligonucleotide antisense to the  
initiation codon, coding region, 5' or 3' end genomic flanking regions,  
5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
junctions of genes encoding a polypeptide associated with lung and/or  
nasal airway dysfunction and a second active agent comprising an  
antifungal steroid and ubiquinone. A composition of the invention  
has anti-inflammatory, anti-allergic, antiasthmatic, hypotensive,  
immunosuppressive, and cytostatic activity. The composition may have a  
use in antisense gene therapy. The composition is useful for treating or  
preventing a respiratory, lung or malignant disease or condition, also  
for enhancing the prophylactic or therapeutic respiratory effect of an  
anti-inflammatory steroid in a subject, for reducing or depleting levels  
of, or reducing sensitivity to adenosine, reducing levels of adenosine  
receptor, producing bronchodilation, increasing levels of ubiquinone or  
lung surfactant in a subject's tissue, or treating bronchoconstriction,  
lung inflammation, lung allergies, or a respiratory disease or condition.  
Note: The sequence data for this patent is not represented in the printed  
specification, but was obtained in electronic format directly from WIPO  
at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 1994 BP; 429 A; 585 C; 633 G; 347 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 8.8e-153 Length: 1994  
Score: 2115.00 Matches: 419  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-377-795-2 (1-419) x ABZ96843 (1-1994)

Db 269 CTGCTTCAGAACAGGCGCTCTCTGAGACCTCCAGCGCTGCCTGGAGGAGATCAAGAG 328  
QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80  
Db 329 CTCGAGATGCCATCCGCGAGAGCAACAGATTCTGCGGAGCGCTCGGAGGAGCTTCTG 388  
QY 81 HisPheGlnAlaSerGlnArgGluGluPheLeuMetCysLysPheGlnGluAla 100  
Db 389 CATTTCCAGCCAGAGAGGAGGAGAGAGTTCTCTCATGTGCAAGTTCCAGGAGGCC 448  
QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120  
Db 449 AGGAAACTGTGTGGAGAGACTCGGCTCGAGAAGCTCGATCTGAAGAGGCGAGAGGAGCAG 508  
QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140  
Db 509 GCTCTGGGGAGGTGGAGCACTGAAGAGATGCCAGCAGAGATGGCTGAGGACAAGGCC 568  
QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160  
Db 569 TCTGTGAAGCCCAAGGTGAGCTCTTGTCTGGGAGCTGCAGAGAGCCAGAGTCGGTTG 628  
QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180  
Db 629 GAGGCTGCCACTAAGGAATGCCAGGCTCTGAGGGTCCGGCCGGCGGCAGCGAGCAG 688  
QY 181 AlaArgGlnLeuGlnSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200  
Db 689 GCGCGGCGAGCTGAGAGTGGAGCGAGGCGCTGCAGCAGCAGCAGCAGCTGCGAGGTGAC 748  
QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220  
Db 749 CAGCTGGCATGCAGGCCAGAGCGCTGGAGCGCGCTCCGCATGGAGCGCCAGCGGCC 808  
QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240  
Db 809 TCGGAGGAGAAGAGGAGCTGGGCCAGTTGCAGTGGCCCTATCACCAGCTCTTCCAAGAA 868  
QY 241 TyrAspAsnHisIleLysSerValValGlySerGluArgLysArgGlyMetGlnLeu 260  
Db 869 TAGCAACACACATCAAGAGACGCTGGTGGCAGTGAGCGGAAGCGAGGAATGCAGCTG 928  
QY 261 GluAspLysGlnGlnLeuGlnGlnAlaGluAlaLeuValAlaLysGlnGluVal 280  
Db 929 GAAGATCTCAACAGCAGCTCCAGCAGGCCCGAGAGGCCCTGTGTGCCAAACAGAGGTTG 988  
QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300  
Db 989 ATCGATAAGCTGAAGGAGGAGCGCAGCAGCAAGATTGTGATGGAGACCGTTCCGGTG 1048  
QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320  
Db 1049 CTGAAGGCCCGAGCGGATATCTCAAGCGCGGATCTCCAGGCTGAGAGGCGCGCGGAG 1108  
QY 321 LysLeuAlaGluLysLysGluLeuLeuGlnGlnGlnLeuGlnArgGluTyr 340  
Db 1109 AACCTGGCCGAGAGAAGGAGCTCTTCAGAGACAGCTGGAGCAGCTGCAGAGGGAGTAC 1168  
QY 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysArgHis 360  
Db 1169 AGCAAACTGAAGGCCAGCTGTCAAGAGTCCGCCAGGATCCAGGACATGAGGAAGCGGCAT 1228  
QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380  
Db 1229 GTCGAGGTCTCCAGGCGCCCTTTGCCCGCCCGCCCTGCCTTCTCTCCCTCCCGGCC 1288  
QY 381 LeuProSerGlnArgSerProProGluProProAspPheCysCysProLysCys 400  
Db 1289 CTGCCAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1348  
QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419

Db 1349 CAGTATCAGGCCCTCATATGGACACCCCTGCAGATACATGTCATGGAGTGCATTGAG 1405  
RESULT 8  
ABV75393  
ID ABV75393 standard; DNA; 1994 BP.  
XX AC ABV75393;  
XX 18-MAR-2003 (first entry)  
DT Human NEMO polypeptide encoding DNA.  
XX  
DE CD40; NF-kappaB essential modulator; NEMO; CYLD; immunosuppressive;  
XX antiinflammatory; cytostatic; gene therapy; human; gene; ds.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH 149..1408  
CDS /\*tag= a  
FT /product= "NEMO"  
FT  
XX WO200292761-A2.  
PN 21-NOV-2002.  
XX 07-MAY-2002; 2002WO-US014570.  
XX 08-MAY-2001; 2001US-00851673.  
PR (IMMV ) IMMUNEX CORP.  
XX Derry JMJ, Fanslow WC, Dougall WC;  
PI WPI; 2003-120669/11.  
DR P-PSDB; ABB82782.  
XX  
PT Identifying compounds that alter one or more biological activities of  
PT CD40 by modulating the binding of NEMO and CYLD, useful for treating  
PT disorders of the immune system, and inflammatory and cancer diseases.  
XX Example 5; Page 33-35; 48pp; English.  
XX The invention relates to methods of identifying compounds that alter one/  
CC more biological activities of CD40. One method involves screening for  
CC molecules that modulate the binding of NF-kappaB essential modulator  
CC (NEMO) and CYLD. The methods and compositions of the invention of  
CC determining compounds that agonize or antagonize a CD40 signaling  
CC activity, are useful for the further definition of CD40-mediated  
CC signaling pathways, and for manipulation of CD40-mediated cellular  
CC responses. They also provide therapeutic agents for treating disorders of  
CC the immune system, and inflammatory and cancer diseases. The present  
CC sequence represents a DNA encoding the human NEMO polypeptide  
XX Sequence 1994 BP; 429 A; 585 C; 633 G; 347 T; 0 U; 0 Other;  
SQ  
Alignment Scores:  
Pred. No.: 8.8e-153 Length: 1994  
Score: 2115.00 Matches: 419  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0  
US-09-377-795-2 (1-419) x ABV75393 (1-1994)  
QY 1 MetAsnArgHisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
Db 149 ATGATAGACCACTCTGGAGAGGCCAACTGTGTGAGATGGTGAGCCCGAGTGTGGCCG 208  
QY 21 AlaAlaAspGlnAspValLeuGluGluSerProLeuGlyLysProAlaMetLeuHis 40  
Db 209 GCAGCAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGGAGGAGCCAGCATGCTGCAC 268



CC thymidines present in the target RNA serves to prevent the breakdown of  
 CC the oligonucleotides into products that free adenosine into the system  
 CC e.g., lung, heart, kidney, etc, tissue environment and thereby, to  
 CC prevent any unwanted effects due to it

XX SQ Sequence 1994 BP; 429 A; 585 C; 633 G; 347 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 8.9e-153 Length: 1994  
 Score: 2115.00 Matches: 419  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 11 Gaps: 0

US-09-377-795-2 (1-419) x ABD20692 (1-1994)

QY 1 MetAsnArgHisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
 Db 149 ATGAATAGGCACCTCTGGAAGAGCCAACTGTGTGAGATGTCGAGCCCACTGTCGTCG 208  
 QY 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysPheAlaMetLeuHis 40  
 Db 209 GCAGCAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGGAAGCCAGCCATGCTGCAC 268  
 QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60  
 Db 269 CTGCTTCAGAACAGGGCGCTCTCGAGACCTCTCCAGCGCTCGCTGGAGGAGATCAAGAG 328  
 QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80  
 Db 329 CTCGAGATGCCATCCGGCAGAGCAACACAGATTCCTCGGAGCGCTGCGAGGAGCTTCG 388  
 QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100  
 Db 389 CATTTCCAGCCAGCCAGAGGAGGAGAGAGAGTTCCTCATGTGCAAGTTCCAGAGAGGCC 448  
 QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120  
 Db 449 AGCAAACTGTGTGAGAGACTCGCGCTGGAGAGCTCGATCTGAAGGCGAGAGGAGCAG 508  
 QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140  
 Db 509 GCTCTCGGAGGTGGAGCACCTGAAAGAGATGTCAGCAGCAGCAGATGCTGAGGACAAAGGCC 568  
 QY 141 SerValIleAlaGlnValThrSerLeuLeuGlyGluLeuGlnGluSerGlnSerArgLeu 160  
 Db 569 TCTGTGAAAGCCAGGTGAGCTCTTGTCTGGGGAGCTGCGAGAGCCAGAGTCGCTTG 628  
 QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180  
 Db 629 GAGGCTGCCACTAAGGATGCGAGGCTCTGGAGGCTCGGGCCCGGCGGCGAGCAGCAG 688  
 QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200  
 Db 689 GCAGCGCAGCTGAGAGTGAAGCGGAGCGCTCAGCAGCAGCAGCAGCAGCTGAGGTGGAC 748  
 QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220  
 Db 749 CAGCTCGCATGCGAGGCGCAGAGCTGGAGGCGCGCTCGCATGAGCGCCAGCGCGCC 808  
 QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240  
 Db 809 TCGGAGAGAGAGAGAGCTGGCCAGTGTGAGTGGCTTATCACCAGCTCTTCCAGAA 868  
 QY 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260  
 Db 869 TACGACAAACCATCAAGAGCAGCTGGTGGGAGTGAAGCGAGCGAGGAGGAGTGCAGCTG 928  
 QY 261 GluAspLeuLysGlnGlnLeuGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280  
 Db 929 GAAGATCTCAAAAGCAGAGCTCCAGCAGGCGGAGGAGGCGCTGTGTGTCGCAACAGAGGAGTG 988

QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300  
 Db 989 ATCGATAAGCTGAAGGAGGAGGCGGAGCAGCACAAGATTGTGTGAGGACCGTTCGGGTG 1048  
 QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320  
 Db 1049 CTGAAGGCCAGCGGATATCTACAAGGCGGACTTCCAGGCTGAGAGGCGGCGGAG 1108  
 QY 321 LysLeuAlaGluLysLysGluLeuLeuGlnGlnGlnLeuGlnLeuGlnArgGluTyr 340  
 Db 1109 AAGCTGGCGAAGAAGAGGAGCTCTTCAGAGGAGCAGCTGGAGCAGCTGCAGAGGAGTAC 1168  
 QY 341 SerLysLeuLysAlaSerCysGlnGluSerAlaArgIleGluAspMetArgLysArgHis 360  
 Db 1169 AGCAAACTGAAGGCCAGCTGTCAAGAGTCGCCAGGATCGCCAGGATGAGAGCGGCAT 1228  
 QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380  
 Db 1229 GTCGAGGTCTCCAGGCGCCCTTGGCCCGCCGCTGCTTCTCTCTCCCTCGGCC 1288  
 QY 381 LeuProSerGlnArgArgSerProGluGluProProAspPheCysCysProLysCys 400  
 Db 1289 CTCCCGAGCAGAGGAGGAGGCCCCCGGAGGAGCCACTTCTGCTGTCCCAAGTGC 1348  
 QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419  
 Db 1349 CAGTATCAGGCCCTCATATGAGACCCCTGCAGATACATGTCATGAGTGCATTGAG 1405

## RESULT 10

AAZ07513  
 ID AAZ07513 standard; DNA; 2009 BP.

XX AAZ07513;

DT 26-NOV-1999 (first entry)

XX Human RIP-associated protein (RAP-2) encoding DNA.

XX Receptor interacting protein; RIP-associated protein-2; RAP-2; RIP;  
 KW inflammation; cell death; cell survival; septic shock; hepatitis;  
 KW graft versus host rejection; diabetes; multiple sclerosis; tumor;  
 KW HIV infection; p55-receptor; FAS-receptor; human; ss.

XX Homo sapiens.

XX WO9947672-A1.

XX 23-SEP-1999.

XX 18-MAR-1999; 99WO-IL000158.

XX 19-MAR-1998; 98IL-00123758.

XX 01-SEP-1998; 98IL-00126024.

XX (YEDA ) YEDA RES & DEV CO LTD.

XX (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.

XX Wallach D, Kovalenko A, Horwitz MS, Li Y;

XX WPI; 1999-562113/47.

XX P-PSDB; AAV27430.

XX New receptor interacting protein-associated protein-2, used to develop  
 PT products for treating, e.g. septic shock, tumors or HIV infection.

XX Claim 4; Fig 1A-B; 132pp; English.

XX This DNA encodes a receptor interacting protein (RIP)-associated protein  
 CC -2 (RAP-2). The RAP-2 proteins, isoforms, analogs, fragments or  
 CC derivatives or DNA can be used for the modulation or mediation of the RIP  
 CC modulated/mediated intracellular effects on the inflammation, cell death  
 CC or cell survival pathways in which RIP is involved directly, or  
 CC indirectly via other modulators/mediators of these pathways. They can be

CC used for treating e.g. septic shock, graft versus host rejection, acute hepatitis, diabetes or multiple sclerosis. They can also be used for treating tumor cells or HIV-infected cells or other diseased cells. The RAP-2 binding proteins can be used for modulating/mediating the function of RAP-2. The products can also be used for diagnostic purposes, e.g. for identifying disorders related to abnormal functioning of cellular effects mediated by the p55-R, FAS-R or other related receptors

SQ Sequence 2009 BP; 418 A; 587 C; 643 G; 356 T; 0 U; 5 Other;

#### Alignment Scores:

Pred. No.: 8.87e-153 Length: 2009  
Score: 2115.00 Matches: 419  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-09-377-795-2 (1-419) x AAZ07513 (1-2009)

QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
DB 154 ATGAATAGGCACCTCTGGAAAGACCAACTGTGTGAGATGTGCGAGCCAGTGTGCGCCG 213  
QY 21 AlaAlaAspGlnAspValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40  
DB 214 GCAGCAGTCAAGACGTACTGGCGAGAGAGTCTCTCTGGGAAGCCAGCCATGCTGCAC 273  
QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60  
DB 274 CTGCTCTCAGAACAGGCGCTCTGAGACCTCCAGCGCTGCTGGAGAGAAATCAAGAG 333  
QY 61 LeuArgAspAlaLeuArgGlnSerAsnGlnLeuLeuArgGluArgCysGluLeuLeu 80  
DB 334 CTCGAGATGCCATCGCGAGAGACCAACAGATTCTCGGGAGCGCTGCGAGAGCTTCTG 393  
QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100  
DB 394 CATTTCCAGCCAGCCAGAGGAGAGAGAGTTCCTCATGTGCAAGTTCAGAGAGGCC 453  
QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120  
DB 454 AGAAATCTGTGGAGAGACTCGGCTTGGAGAGTCTGATCTCAAGAGGCGAGAAGAGCAG 513  
QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140  
DB 514 GCTCTCGGAGGTGGAGACACCTGAAGATGCCAGCAGATGGCTGAGGACAGGCC 573  
QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGluSerGlnSerArgLeu 160  
DB 574 TCTGTGAAGCCAGGTGACGCTCTTGTCTCGGGAGCTGCGAGAGCCAGAGTCGCTTG 633  
QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaAlaSerGluGln 180  
DB 634 GAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGCTCGGGCCCGGCGCCAGCAGCAG 693  
QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200  
DB 694 GCGCGGACGTGGAGAGTGAAGCGCGAGGCGCTGCGAGCAGCAGCAGGTGAGGTGAC 753  
QY 201 GlnLeuArgMetGlnGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220  
DB 754 CAGCTCGCATGTCAGGGCCAGAGCGTGGAGGCGCGCTCCGATGGAGCGCCAGCGCCG 813  
QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaThrHisGlnLeuPheGlnGlu 240  
DB 814 TCGAGAGAGAGAGGAGTGGCCAGTTCAGAGTGGCTTATCACCAGCTCTTCCAGAA 873  
QY 241 TyrAspAsnHisLeuLysSerValValGlySerGluArgLysArgGlyMetGlnLeu 260  
DB 874 TAGCAACAACACATCAAGAGCAGCTGTGTGGCAGTGGAGCGGAGCGAGGATCGAGTG 933  
QY 261 GluAspLeuLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280

DB 934 GAAGATCTCAAAACAGCAGCTCCAGCAGCGCAGGAGGCCCTGGTGCCTCAACAGAGAGTG 993  
QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300  
DB 994 ATCGATAAGCTGAAGAGAGGAGCGCCAGCAGCAAGATTGTATGGAGACCGTTCCGGTG 1053  
QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320  
DB 1054 CTGAAGGCCCGAGGGGATATCTACAAGGGGACTTCCAGGCTGAGAGGCGAGCCCGGAG 1113  
QY 321 LysLeuAlaGluLysLysGluLeuLeuGlnGlnLeuGlnLeuGlnArgGluTyr 340  
DB 1114 AAGCTGGCCGAGAAAGAGAGCTCTTCGAGGAGCAGCTGGAGCAGCTGCAGAGGAGTAC 1173  
QY 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysArgHis 360  
DB 1174 AGCAACTGAAGGCCAGCTGTGAGGATCGGCGAGATCGAGGACATGAGGAGCGGCAT 1233  
QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380  
DB 1234 GTCGAGGTCTCCAGGCCCTTGCCCCCGCCCTGCTACCTCTCTCTCTCTCTCTCTCTCT 1293  
QY 381 LeuProSerGlnArgArgSerProProGluGluProProAspPheCysCysProLysCys 400  
DB 1294 CTGCCCAGCCAGAGAGAGGCCCGCCCGAGAGGCCACCTGACTTCTGTGTCTCCCAAGTC 1353  
QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419  
DB 1354 CAGTATCAGGCCCTGATATGGACACCTGCGATACATGTCATGAGTGCATTGAG 1410  
RESULT 11.  
ACD23012  
ID ACD23012 standard; cDNA; 2035 BP.  
XX  
AC ACD23012;  
XX  
DT 25-AUG-2003 (first entry)  
XX  
DE Human NEMO cDNA.  
XX  
KW Human; Gene; ss; NF-kappaB essential modulator; nuclear factor kappa B;  
KW incontinentia pigmenti; X-linked disorder; chromosome Xq28; NEMO;  
KW immunomodulatory; dermatological; osteopathic; neuropathic;  
KW apoptosis-related disease; immune-system related disease;  
KW blood vessel-related disease; skin defect; dental defect; osteopetrosis;  
KW ophthalmologic defect; neurological defect.  
XX  
OS Homo sapiens.  
XX  
FN US2003032055-A1.  
XX  
PD 13-FEB-2003.  
XX  
PF 22-MAY-2001; 2001US-00863049.  
XX  
PR 22-MAY-2000; 2000US-0206223P.  
XX  
PA (KENW/) KENNRICK S J.  
PA (WOFF/) WOFFENDIN H.  
PA (MUNN/) MUNNICH A.  
PA (SMAH/) SMAHI A.  
PA (ISRA/) ISRAEL A.  
PA (POUS/) POUSTKA A.  
PA (HEIS/) HEISS N.  
PA (DURS/) D'URSO M.  
PA (LEWI/) LEWIS R A.  
PA (NELS/) NELSON D L.  
PA (ARAD/) ARADHYA S.  
PA (LEVY/) LEVY M.  
XX  
PI Kenrick SJ, Woffendin H, Munnich A, Smahi A, Israel A;  
PI Poustka A, Heiss N, D'urso M, Lewis RA, Nelson DL, Aradhy S;

PI Levy M;  
 XX WPI: 2003-492063/46.  
 DR P-PSDB; ABO17485.  
 XX  
 PT Detection of necrosis factor-kappa B related medical condition in  
 PT organism, by obtaining sample from the organism, and analyzing the sample  
 PT for alteration in specified amino acid sequences.  
 XX  
 XX Disclosure; Page: 44pp; English.  
 XX  
 CC The invention relates to a nuclear factor-kappa B (NF-kappa B) related  
 CC medical condition in an organism being detected by obtaining a sample  
 CC from the organism, and analyzing the sample for an alteration in a the  
 CC nuclear factor kappaB essential modifier (NEMO) gene or protein sequence  
 CC (neither shown in the specification). The alteration results in  
 CC inactivation of NF-kappa B. Also included are treating or preventing NF-  
 CC kappa B related medical condition in an organism by administering the  
 CC NEMO protein to the organism and screening a test organism for a compound  
 CC for the treatment of NF-kappa B related medical condition (by  
 CC administering the compound to the organism, and assaying for an  
 CC improvement in the NF-kappa B related medical condition). The method  
 CC useful is for detecting NF-kappa B related condition, e.g. incontinentia  
 CC pigmenti (IP), apoptosis-related disease, immune-system related disease,  
 CC blood vessel-related disease, skin defect, dental defect, osteopetrosis,  
 CC ophthalmologic defect, or neurologic defect, in an organism, i.e. human  
 CC including affected individual, carrier individual, or noncarrier  
 CC individual. The NEMO gene is located on chromosome Xq28, incontinentia  
 CC pigmenti being an X-linked disorder. Experiments in this study show  
 CC variations in exon 2, 10, 9 and particularly intron 3 to be linked to  
 CC familial incontinentia pigmenti. The present sequence is the human NEMO  
 CC cDNA. Note: The present sequence is not shown in the specification but  
 CC was obtained from Genbank using the reference number given in the  
 CC specification  
 XX  
 SQ Sequence 2035 BP; 425 A; 592 C; 637 G; 381 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9, 01e-153 Length: 2035  
 Score: 2115.00 Matches: 419  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0  
 US-09-377-795-2 (1-419) x ACD23012 (1-2035)  
 QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
 DB 186 ATGAATAGGCACCTCTGGAAGAGAGCAACTGTGTGAGATGGTGCGAGCCAGTGGTGGCCCG 245  
 QY 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40  
 DB 246 GCAGCAGATCAGACGCTACTGGCGGAAGAGTCTCTCTGGGGGAAGCAGCCATGCTGCAC 305  
 QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60  
 DB 306 CTGCCTTCAGAACAGGGCGCTCTTGAGACCTTCAGCGCTGCTGGAGGAGATCAAGAG 365  
 QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80  
 DB 366 CTCGGAGATGCCATCCGGCAGAGCAACAGATTCTCGGGAGCGCTGCGAGGAGCTTCG 425  
 QY 81 HisPheGlnAlaSerGlnArgGluGlyLysGluPheLeuMetCysLysPheGlnGluAla 100  
 DB 426 CATTTCCAGCCAGCCAGAGGGAGAGAGAGTTCCTCATGTGCAAGTTCCAGGAGGCC 485  
 QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120  
 DB 486 AGGAAACTGTGTGAGAGACTCGGCCCTGGAGAACTGATCTGAAGAGGAGCAGAGGAGCAG 545  
 QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140  
 DB 1442  
 Db 546 GCTCTCGGGAGGTGGAGCAGCACCTGAAGAGATGCCAGCAGCAGATGGCTGAGGACAAGGCC 605  
 QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGluSerGlnSerArgLeu 160  
 Db 606 TCTGTGAAAGCCAGGTGAGCTCTTCTGCTGGGGAGCTGCGAGGAGAGCCAGAGTCTGCTTG 665  
 QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180  
 Db 666 GAGGCTGCCACTAAGGANTGCCAGGCTCTGGAGGGTGGGCCCGGGCGGCGAGGAGCAG 725  
 QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200  
 Db 726 GCGCGCAGCTGGAGAGTGGAGCGAGGCGCTGCGAGCAGCAGCAGCAGCGTGCAGTGGAC 785  
 QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220  
 Db 786 CAGCTCGCATGTCAGGGCCAGAGCGTGGAGGGCGCGCTCCGCATGGAGCGCCAGGCGGCC 845  
 QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240  
 Db 846 TCGGAGGAGAGAGGAGAGTGGCCAGTGGAGTGGCTTATCACCAGCTCTTCCAAGAA 905  
 QY 241 TyrAspAsnHisLysSerValValGlySerGluArgLysArgGlyMetGlnLeu 260  
 Db 906 TAGCAACAACACATCAAGAGCAGCGTGGTGGGCAGTGAGCGGAAGCAGGAATGCAGCTG 965  
 QY 261 GluAspLeuLysGlnGlnLeuGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280  
 Db 966 GAAGATCTTCAACAGCAGCTCCAGCAGGCGGAGGAGGCGCTGGTGCCCAACAGGAGGTG 1025  
 QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300  
 Db 1026 ATCGATACTGAAGAGGAGGCGGCGGAGCAGCAGCAAGATTGTGATGAGACCTGTCGGTG 1085  
 QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320  
 Db 1086 CTGAAGGCCAGCGGATATCTACAAGCGGACTTCCAGGCTGAGAGGAGCGCCGCGAG 1145  
 QY 321 LysLeuAlaGluLysLysGluLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGluTyr 340  
 Db 1146 AAGCTGGCGAGAGAGAGAGTCTCTGCGAGGAGCAGCTGGAGCAGCTGCGAGGAGATC 1205  
 QY 341 SerLysLeuLysAlaSerCysGlnGluSerAlaArgIleGluAspMetArgLysArgHis 360  
 Db 1206 AGCNAACTGAGGCCAGCTGTGAGGAGTGGCCAGGATCGAGACATGAGGAAGCGCAT 1265  
 QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380  
 Db 1266 GTCGAGGTCTCCAGGCCCTTGGCCCGCCCTTACCTCTCTCTCTCTCTCTCTCTCTCT 1325  
 QY 381 LeuProSerGlnArgArgSerProGluGluProProAspPheCysCysProLysCys 400  
 Db 1326 CTGCCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1385  
 QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419  
 Db 1386 CAGTATCAGGCCCTGATATGACACCTTCAGATACATGTCTATGAGTGATGATGAG 1442  
 RESULT 12  
 AAA35028  
 ID AAA35028 standard; DNA; 8631 BP.  
 XX  
 AC AAA35028;  
 XX  
 DT 28-JUL-2000 (first entry)  
 XX  
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2717.  
 DE  
 DE Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphorothioate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;

KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukemia; lymphoma; carcinoma; metastasis; ss.  
 XX Homo sapiens.  
 OS WO200009525-A2.  
 PN 24-FEB-2000.  
 PD 03-AUG-1999; 99WO-US017712.  
 XX 03-AUG-1998; 98US-0095212P.  
 PR (UYEC-) UNIV EAST CAROLINA.  
 PA  
 XX Nyce JW;  
 PI WPI; 2000-205971/18.  
 DR  
 XX New antisense oligonucleotides useful for treating e.g. pulmonary  
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 PT cancers.  
 XX  
 XX Disclosure; Page 969-971; 1343pp; English.  
 PS  
 XX The present invention describes a new composition comprising an antisense  
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
 CC nucleic acids involved in bronchoconstriction, allergies, and/or  
 CC inflammation. The ON can have antiinflammatory, antiallergic,  
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
 CC useful for the treatment of diseases associated with inflammation,  
 CC impaired airways, including lung disease and diseases whose secondary  
 CC effects afflict the lungs of a subject. They can be used for treating  
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
 CC impeded respiration, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,  
 CC carcinomas, and cancers which may metastasize to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of the  
 CC ONs reduces side effects. The A-containing ONs break down with the  
 CC release of deoxyadenosine which activates adenosine receptors causing  
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
 CC nucleotide sequences given in the sequence listing from the present  
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
 CC Sequences given in the disclosure of the present invention do not match  
 CC up with their corresponding SEQ ID NO.: sequences given in the sequence  
 CC listing  
 XX  
 SQ Sequence 8631 BP; 2280 A; 2050 C; 2270 G; 2031 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 4,95e-152 Length: 8631  
 Score: 2115.00 Matches: 419  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0  
 US-09-377-795-2 (1-419) x AAA35028 (1-8631)  
 QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
 DB 6786 ATGAATAGGACCTCTGGAAAGAGCAACTGTGTGATGGTGCAGCCAGTGGTGGCCG 6845  
 QY 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40  
 DB 6846 GCAGCAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGGAAGCCAGCCATGCTGCAC 6905

QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGlnGlnGlu 60  
 DB 6906 CTGCCTTCAGAACACAGGGCGCTCTTGAGACCTCTCCAGCGCTGCCTGAGGAGATCAAGAG 6965  
 QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeu 80  
 DB 6966 CTCGAGATGTCATCCGGCAGAGCAACCAAGATTCGCGGAGCGCTGCGAGAGGCTCTTG 7025  
 QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100  
 DB 7026 CATTTCCAGCCAGCCAGAGGAGAGAGAGTTCCTCATGTGCAAGTTCCAGAGAGGCC 7085  
 QY 101 ArgLysLeuValGluArgLeuGlyLeuLysLeuAspLeuLysArgGlnLysGluGln 120  
 DB 7086 AGGAAACTGTGTGAGAGACTCGGCTCGAGAAAGCTCGATCTGAAGAGGCAGAGGAGCAG 7145  
 QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140  
 DB 7146 GCTCTGGGGAGGTGGAGCACCTGAAGAGATGCCAGAGCAGATGGCTGAGGACAGGCC 7205  
 QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160  
 DB 7206 TCTGTGAAAGCCAGGTGACGTCTTGTCTGGGGAGCTGCAGGAGAGCCAGAGTGCCTTG 7265  
 QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180  
 DB 7266 GAGCTCTCCACTAAGGAATGCCAGGCTCTGGAGGCTGGGGCCCGGCGCCAGCGAGCAG 7325  
 QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200  
 DB 7326 GCGCGGAGCTGGAGAGTGAGCGCGAGCGCTGCAGCAGCAGCAGCAGCTGCAGGTGGAC 7385  
 QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220  
 DB 7386 CAGCTGCGCATCAGGGCCAGAGCTGGAGCGCGCTCCGCATGTGAGCGCCAGCGCCGCC 7445  
 QY 221 SerGluGlyLysArgLysLeuAlaGlnLeuValAlaThrHisGlnLeuPheGlnGlu 240  
 DB 7446 TCGAGGAGAGAGAGAAAGCTGGCCCACTGTGAGGTGCGCTATCACCAGCTCTTCCAAAG 7505  
 QY 241 TyrAspAsnHisIleLysSerSerValValLysSerGluArgLysArgGlyMetGlnLeu 260  
 DB 7506 TACGACAACACACATCAAGAGCAGCGTGTGGCAGTGCAGCGAAGCAGAGGATGCAGCTG 7565  
 QY 261 GluAspLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280  
 DB 7566 GAAGATCTCAACAGCAGAGCTCCAGCAGCGCAGGAGGCGCTGTGGTGGCCAAACAGAGGTG 7625  
 QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300  
 DB 7626 ATCGATNAAGCTGAAGGAGGAGGCGGAGCAGCAGCAAGATTGTGATGGAGACCGTTCGGGTG 7685  
 QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320  
 DB 7686 CTGAAGGCCAGCGCGATATCTCAAGCGGACTTCCAGGCTGAGAGCGAGCGCCCGGAG 7745  
 QY 321 LysLeuAlaGluLysGluLeuLeuGlnGlnGlnLeuGlnLeuGlnArgGluTyr 340  
 DB 7746 AAGCTGCGCGAGAGAGAGGAGTCTCTGAGGAGCAGCTGAGGAGCAGCTGCAGAGGAGGTAC 7805  
 QY 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysArgHis 360  
 DB 7806 AGCAAACTGAAGGCCAGCTGTCAAGAGTCCGCCAGGATCCAGGACATGAGGAGCGGCAT 7865  
 QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380  
 DB 7866 GTGAGGTCTCCAGAGCCCTTTGCCCGCCCTGCTACCTCTCTCTCTCTCTCTCTCTCTCT 7925  
 QY 381 LeuProSerGlnArgArgSerProGluGluProProAspPheCysCysProLysCys 400  
 DB 7926 CTCGCCAGCAGAGAGAGAGCCCCCGAGAGCCACTGACTTCTGCTGTCTCCCAAGTGC 7985  
 QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419





Db 7626 ATCGATAGCTGAAGGAGGCGGAGCAGACAAAGATTGTGATGAGACCGTTCGGGTG 7685  
QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaArgGlnAlaArgGlu 320  
Db 7686 CTGAAGGCCAGGCGGATATCTCAAGCGGACTTCCAGGCTGAGAGGCGAGCCCGGAG 7745  
QY 321 LysLeuAlaGluLysLysGluLeuLeuGlnGluGlnLeuGlnLeuGlnArgGluTyr 340  
Db 7746 AAGTGGCCGAGAGAGAGGAGCTCTGTCAGAGCAGCTGAGCAGCTGAGAGGAGTAC 7805  
QY 341 SerLysLeuLysAlaSerCysGlnGluSerAlaArgIleGluAspMetArgLysArgHis 360  
Db 7806 AGCAACTGAAGGCCAGCTGTGAGAGTGGCCGAGATCGAGACATGAGGAGCGCAT 7865  
QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380  
Db 7866 GTCGAGGTCTCCAGGCCCTTGGCCCGCCCTGCTACCTCTCTCCCTGGCC 7925  
QY 381 LeuProSerGlnArgArgSerProGluGluProProAspPheCysCysProLysCys 400  
Db 7926 CTGCCAGCAGAGGAGGAGGCCCCCGAGGAGCCACCTGACTTCTGCTGCCAAGTGC 7985  
QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419  
Db 7986 CAGTATCAGGCCCTGATATGGACACCTCGACATACATGTCTAGGATGCAATTGAG 8042

## RESULT 14

AB296844

ID AB296844 standard; DNA; 8631 BP.

AC AB296844;

17-OCT-2003 (first entry)

Human nucleic acid sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction;  
antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;  
antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
antisense gene therapy; respiratory; lung; adenosine sensitivity;  
adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIC-) EPIGENESIS PHARM INC.

Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

Pi Miller S, Tang L, Shahabuddin S;

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired  
respiration, has oligo(s) antisense to specific gene(s) or its  
corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
ubiquinone.

Disclosure; SEQ ID NO 12086; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a  
first active agent comprising an oligonucleotide antisense to the  
initiation codon, coding region, 5' or 3' end genomic flanking regions,  
5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
junctions of genes encoding a polypeptide associated with lung and/or

nasal airway dysfunction and a second active agent comprising an  
antiinflammatory steroid and ubiquinone. A composition of the invention  
has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive, and  
immunosuppressive, and cytostatic activity. The composition may have a  
use in anisense gene therapy. The composition is useful for treating or  
preventing a respiratory, lung or malignant disease or condition, also  
for enhancing the prophylactic or therapeutic respiratory effect of an  
antiinflammatory steroid in a subject, for reducing or depleting levels  
of, or reducing sensitivity to adenosine, reducing levels of adenosine  
receptor, producing bronchodilation, increasing levels of ubiquinone or  
lung surfactant in a subject's tissue, or treating bronchoconstriction,  
lung inflammation, lung allergies, or a respiratory disease or condition.  
Note: The sequence data for this patent is not represented in the printed  
specification, but was obtained in electronic format directly from WIPO  
at ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 8631 BP; 2280 A; 2050 C; 2270 G; 2031 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 4,95e-152 Length: 8631  
Score: 2115.00 Matches: 419  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-09-377-795-2 (1-419) x AB296844 (1-8631)

QY 1 MetAsnArgHisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
Db 6786 ATGATAGGACCTCTGGAGAGCAACTGTGTAGATGTGTGACCCCGGTGGCCG 6845  
QY 21 AlaAlaAspGlnAspValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40  
Db 6846 GCAGCAGATCAGGACGTACTGGCGAAGAGTCTCTCTGGGAAAGCCAGCATGCTGCAC 6905  
QY 41 LeuProSerGlnGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGlnGlnGlu 60  
Db 6906 CTGCTCTTCAAGAACAGGCGCTCTCTGAGACCTCTCCAGCGCTCCCTGGAGGAGAAATCAAGAG 6965  
QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80  
Db 6966 CTCCGAGATGCCATCCGCGCAGAGCAACAGATCTCTCGGGAGCGCTGCGAGAGCTTCTG 7025  
QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGlnAla 100  
Db 7026 CATTTCCAGGCCAGCCAGAGGAGGAGAGAGAGTCTCTCATGTGCAAGTTCCAGAGGCC 7085  
QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGlnGln 120  
Db 7086 AGGAACTGTGTGAGAGACTCGGCTGGAGAGCTCGATCTGAAGAGCCAGAGGAGCAG 7145  
QY 121 AlaLeuArgGluValGluHisLeuLysLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140  
Db 7146 GCTCTCGGAGAGGTGGAGCACCCTGAAGAGATGCCAGCAGCAGATGGCTGAGCAAGGCC 7205  
QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerArgLeu 160  
Db 7206 TCTGTGAAGGCCAGGTGAGCTCTTGTCTGGGAGCTGCGAGAGAGCCAGAGTCTGCTT 7265  
QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180  
Db 7266 GAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGTTCGGGCGGCGGCGGCGAGCAG 7325  
QY 181 AlaArgGlnLeuGlnSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValasp 200  
Db 7326 GCGCGCAGCTGGAGAGTGAAGCGCGGCGCTGCAGCAGCAGCAGCAGCGTGTGAGTGCAC 7385  
QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220  
Db 7386 CAGCTGGCATGTCAGGCGCCAGAGCTGGAGGCCCGCGCTCCGCATGGAGCGCCAGCGCC 7445  
QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240

Db 7446 TCGAGGAGAGAGGAGCTGGCCAGCTTGCGAGTGGCTTATCACAGCTCTTCCAGAA 7505  
Qy 241 TyraAspHisLleLysSerValValGlySerGluArgLysArgGlyMetGlnLeu 260  
Db 7506 TACGACAAACACATCAAGAGAGCGCTGGTGGCGAGTGGAGCGGAGGAGGAGTGCAGCTG 7565  
Qy 261 GluAspLeuLysGlnGlnLeuGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280  
Db 7566 GRAGATCTCAACAGCAGCTCCAGCAGCGCCGAGGAGGCGCTTGTTGGCCAAACAGGAGGTG 7625  
Qy 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysLysValMetGluThrValProVal 300  
Db 7626 ATCGATAAGCTGAAGGAGGAGCGCCAGCAGCACAAAGATTGTGATGGAGACCGTTCGGGTG 7685  
Qy 301 LeuLysAlaGlnAlaAspLleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320  
Db 7686 CTGAAGGCCCGAGGCGGATATCTACAAGCGGACTTCAGGCTGAGAGCGAGGCCCGGAG 7745  
Qy 321 LysLeuAlaGluLysLysGluLeuGlnGlnGlnLeuGlnLeuGlnArgGluTyr 340  
Db 7746 AAGCTGGCCGAGAGAGGAGCTCTTCAGGAGCAGCTGGAGCAGCTGCAGAGGGAGTAC 7805  
Qy 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgLysGluAspMetArgLysArgHis 360  
Db 7806 AGCAAACTGAAGGCCAGCTGTCAAGGAGTGGCCAGGATCGAGGACATGAGGAAGCGCAT 7865  
Qy 361 ValGluValSerGlnAlaProLeuProAlaProAlaProAlaProAlaProAlaProLeuAla 380  
Db 7866 GTCGAGGTCTCCAGGCCCGCCCTTGGCCCGCCCGCCCTGCTTCTCTCTCTCTCTCTCTCT 7925  
Qy 381 LeuProSerGlnArgArgSerProGluGluProGluGluProGluGluProGluGluProLysCys 400  
Db 7926 CTGCCAGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7985  
Qy 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnHisValMetGluCysLysLeuGlu 419  
Db 7986 CAGTATCAGGCCCTGTATGGACACCCCTGCAGATACATGTCATGGAGTGCATTGAG 8042

RESULT 15  
ABD20693  
ID ABD20693 standard; DNA; 8631 BP.  
XX AC ABD20693;  
XX DT 29-JUL-2004 (first entry)  
XX DE Human pulmonary and inflammatory target DNA #304.  
XX KW Human; antiseize; bronchoconstriction; allergy; hyposecretion; pain;  
XX KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
XX KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;  
XX KW analgesic; hypotensive; immunosuppressive; cycostatic; cystic fibrosis;  
XX KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
XX KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
XX KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
XX KW pulmonary transplantation rejection; ds.  
XX OS Homo sapiens.  
XX PN WO200285309-A2.  
XX PD 31-OCT-2002.  
XX PF 23-APR-2002; 2002WO-US013143.  
XX PR 24-APR-2001; 2001US-0286036P.  
XX PA (EPIG-) EPIGENESIS PHARM INC.  
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
XX PI Miller S, Tang L, Shahabuddin S;

DR WPI; 2003-093058/08.  
XX Pharmaceutical composition for treating asthma, has antiseize  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.  
XX Claim 15; SEQ ID NO 12086; 763pp; English.  
PS This invention describes a novel composition (a) a first active agent,  
XX comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has antiallergic, antiinflammatory, antiasthmatic, is a  
CC analgesic, hypotensive, immunosuppressive and cycostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to  
CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymidines present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it  
XX  
SQ Sequence 8631 BP; 2280 A; 2051 C; 2270 G; 2030 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 4,95e-152 Length: 8631  
Score: 2115.00 Matches: 419  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 11 Gaps: 0

US-09-377-795-2 (1-419) x ABD20693 (1-8631)

Qy 1 MetAsnArgHisLeuTyrLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
Db 6786 ATGAATAGGACCCCTCTGGAAGAGCCCACTGTGTGAGATGTTGCGAGCCAGTGGTGGCCG 6845  
Qy 21 AlaAlaAspGlnAspValLeuGluGluSerProLeuGlyLysProAlaMetLeuHis 40  
Db 6846 GCAGCAGATCAGACACGTACTTGGGCGAAGAGTCTCTCTGGGGAAGCCAGCATGCTGTCAC 6905  
Qy 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluAsnGlnGlu 60  
Db 6906 CTGCCTTCAGACAGAGGCGCTCTTGAGACCTTCAGCGCTGCTCGAGGAGATCAAGAG 6965  
Qy 61 LeuArgAspAlaLysArgGlnSerAsnGlnLysLeuArgGluArgCysGluGluLeu 80  
Db 6966 CTCGAGATGCCATCCCGCAGACCAACAGATTTCTCGGAGCGCTGCGAGGAGCTTCTG 7025  
Qy 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100  
Db 7026 CATTTTCAAGCCAGCCAGAGGAGGAGAGGAGTCTCTCATGTGCAAGTTTCCAGGAGGCC 7085  
Qy 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120

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|||||
Db 7086 AGGAACTGGTGGAGAGCTCGGCTCGAGAGCTCGATCTGAAGAGCGCAAGAGGACAG 7145
QY 121 AlalaArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140
|||||
Db 7146 GCTCTGGCGGAGTGGAGACCTCAAGAGATGCCAGCAGCAGATGCTGAGGACAAAGGCC 7205
QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnLysSerArgLeu 160
|||||
Db 7206 TCTGTGAAGCCCAAGGTGAGCTCTTCTCGGGAGCTGCAGAGAGCCAGAGTGCCTTG 7265
QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
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QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnHisSerValGlnValAsp 200
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QY 221 SerGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240
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QY 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260
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QY 261 GluAspLeuLysGlnGlnLeuGlnAlaGluAlaLeuValAlaLysGlnGluVal 280
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QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300
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QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320
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QY 321 LysLeuAlaGluLysLysGluLeuLeuGlnGlnLeuGlnLeuGlnArgGluTyr 340
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Db 7746 AAGCTGGCCGAGAAGAGAGCTCTTCAGGAGCAGCTGCAGCAGCTGCAGAGGGAGTAC 7805
QY 341 SerLysLeuLysAlaSerCysGlnGluSerAlaArgIleGluAspMetArgLysArgHis 360
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QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380
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QY 381 LeuProSerGlnArgArgSerProGluGluProProAspPheCysCysProLysCys 400
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Db 7926 CTGCCCCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7985
QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
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Search completed: February 9, 2005, 03:30:18  
Job time : 758 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 9, 2005, 02:52:33 ; Search time 4378 Seconds  
(without alignments)  
3642.971 Million cell updates/sec

Title: US-09-377-795-2

Perfect score: 2115

Sequence: 1 MNRHLKSQLCEMVQPSGGP.....COYQAPDMDTLQIHVMCEIE 419

Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q/cgn2\_1/USPTO\_spool/US0377795/runat\_07022005\_112551\_12131/app\_query.fasta\_1.583  
-DB=EST -Qfmt=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bites -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
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-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2115	100.0	1958	3	CR600010 full-leng
2	2115	100.0	1960	3	BC046922 Homo sapi
3	2099.5	99.3	1962	6	CA916723 K142FL hu
4	2086.5	98.7	1943	3	CR604149 full-leng
5	1840.5	87.0	1751	3	CR603029 full-leng
6	1813	85.7	4535	3	AK037020 Mus muscu
7	1412.5	66.8	1118	5	EX332283
8	1322	62.5	974	1	AL545822
9	1308.5	61.9	1043	1	AL541141

10	1253.5	59.3	957	5	BQ932422
11	1247	59.0	919	1	AL547021
12	1245.5	58.9	1098	4	BM478785
13	1235	58.4	1024	1	AL558226
14	1225	57.9	1011	5	BX325316
15	1208.5	57.1	920	5	BX418246
16	1206	57.0	1098	4	BM473416
17	1205	57.0	975	5	BX418245
18	1200	56.7	925	5	BX328265
19	1194	56.5	902	5	BQ944161
20	1150	54.4	872	5	BX418606
21	1135.5	53.7	1091	4	BM467195
22	1123.5	53.1	929	5	BU528711
23	1120	53.0	942	5	BU930960
24	1118.5	52.9	963	1	AL526920
25	1093	51.7	768	7	CN460471
26	1093	51.7	870	5	BQ956152
27	1090	51.5	1140	4	BM546491
28	1084	51.3	757	7	CO433136
29	1070	50.6	1051	5	BQ056837
30	1066.5	50.4	1056	5	BQ057044
31	1060	50.1	634	7	CV025468
32	1055.5	49.9	730	5	BU708502
33	1053	49.8	758	4	BI765235
34	1052.5	49.8	994	5	BQ716889
35	1045.5	49.4	781	7	CK639928
36	1045	49.4	951	5	BQ064520
37	1039	49.1	764	7	CN460413
38	1027	48.6	1164	3	CR612085
39	1023	48.4	781	5	BX398053
40	1019.5	48.2	815	5	BX324969
41	1014	47.9	923	4	BM559994
42	1011.5	47.8	686	7	CK636315
43	1010.5	47.8	733	5	BQ771466
44	1008	47.7	789	6	CB521645
45	1001.5	47.4	1201	2	BE273489

#### ALIGNMENTS

RESULT 1	CR600010	1958 bp	mRNA	linear	HTC 21-JUL-2004
LOCUS	CR600010	full-length cDNA clone CS0DL002VJ17 of B cells			(Ramos cell line)
DEFINITION	CR600010	Cot 25-normalized of Homo sapiens			(human).
ACCESSION	CR600010.1	GI:50480817			
VERSION	HTC; CNSLT	cDNA.			
KEYWORDS	Homo sapiens	(human)			
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1	(bases 1 to 1958)			
AUTHORS	Li, W.B., Gruber, C., Jesse, J., and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue				
REFERENCE	2	(bases 1 to 1958)			
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)				
COMMENT	- Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime ends enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.				
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source	1. .1958				
	/organism="Homo sapiens"				

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ORIGIN
Alignment Scores:
Pred. No.: 5,08e-182 Length: 1958
Score: 2115.00 Matches: 419
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-377-795-2 (1-419) x CR600010 (1-1958)

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Db 144 ATGATAGGACCTCTGGAAGACCAACTGTGTGATGTGCGACCCAGTGGTGGCCGG 203
QY 21 AlalaAspGlnAspValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40
Db 204 GCAGCAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGGAAGCCAGCCATGCTGCAC 263
QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluAsnGlnGlu 60
Db 264 CTGCTTCAGAACAGGGCGCTCTCTGAGACCTCCAGCGCTGCGTGGAGAGAAATCAAGAG 323
QY 61 LeuArgAspAlaLeuArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80
Db 324 CTCGAGATGCCATCGCGCAGACACACAGATTCTCGGGAGCGCTGCGAGAGCTTCTG 383
QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
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QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120
Db 444 AGGAACCTGTGTGAGAGACTCGGCCCTGGAGAGCTCGATCTGAAGAGGCGAAGAGGAG 503
QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140
Db 504 GCTTCGGGAGGTGGAGCAGCCTGAAGAGATGCCAGCAGCAGATGGCTGAGGACAGGCC 563
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Db 564 TCTGTGAAGCCAGGTGAGTCTCTCTGCGGGAGCTGCGAGGAGCAGAGTGCCTTG 623
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QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419
Db 1344 CAGTATCAGGCCCTGTATGTGACACCTCGCAGATACATGTGATGAGTGCATTGAG 1400

RESULT 2
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LOCUS Homo sapiens inhibitor of kappa light polypeptide gene enhancer in
DEFINITION B-cells, kinase gamma, mRNA (cdna clone IMAGE:5476394), containing
frame-shift errors.
ACCESSION BC046922
VERSION BC046922.1 GI:28422142
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1960)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, R.K., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
JOURNAL MEDLINE
PUBMED 22388257
REFERENCE 2 (bases 1 to 1960)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (14-FEB-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

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## COMMENT

Contact: MGC help desk  
 Email: cgabs-xemail.nih.gov  
 Tissue Procurement: DCTD/DTF  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: nisc.mgc@nih.gov  
 Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,  
 Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,  
 Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 44 Row: 1 Column: 23  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 21361093  
 This clone has the following problem: frame shifted.

## FEATURES

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## ORIGIN

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 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

US-09-377-795-2 (1-419) x BC046922 (1-1960)

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 DB 176 GCAGCAGATCAGGACGCTACTGGGGAGAGAGTCTCTCTGGGGAGCCAGCCATGCTGCAC 235  
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 QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60  
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 QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80  
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## RESULT 3

## CA916723

## LOCUS

## DEFINITION

## K142FL human keratinocyte matchmaker cDNA library Homo sapiens CDNA

## clone K142 5' similar to IKK gamma/ NEMO, mRNA sequence.

## ACCESSION

## CA916723.1

## VERSION

## GI:28951960

## KEYWORDS

## EST.

## SOURCE

## Homo sapiens (human)

## ORGANISM

## Homo sapiens

## Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

## Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

## 1 (bases 1 to 1962)

## AUTHORS

## Scarafia, L.E., Stouffer, S.D. and Swinney, D.C.

## TITLE

## Identification of Ring Finger proteins that interact with Ubch5a,



JOURNAL COMMENT

an ubiquitin-conjugating enzyme  
Unpublished (2002)  
Contact: Scarafia LE  
Enzymology  
Roche Bioscience  
3401 Hillview Ave, S3-1, Palo Alto, CA 94304-1397, USA  
Tel: 650 354 7997  
Fax: 650 354 7554  
Email: liliana.scarafia@roche.com  
Full length single stranded sequencing of baited insert  
Insert Length: 2000 Std Error: 0.00  
Seq primer: primer 2 (5395)TACCACCTACAATGGATG; and insert-specific  
POLYA-Yes.

FEATURES

Location/Qualifiers

1..1962  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="K142"  
/cell\_type="keratinocyte"  
/cell\_line="HaCat cell line; derived from long term primary  
human adult skin keratinocyte"  
/lab\_host="yeast/E.coli"  
/clone\_lib="human keratinocyte matchmaker cDNA library"  
/note="Vector: pACT2; Site 1: EcoRI; Site 2: XhoI;  
Matchmaker yeast two-hybrid system from Clontech; pACT2  
vector has GAL4 AD and HA epitope under ADH1 promoter.  
This oligo-dr primed library was screened with human  
Ubch5a as bait, to obtained interacting proteins."

## ORIGIN

Alignment Scores:

Pred. No.: 1 32e-180 Length: 1962  
Score: 2099.50 Matches: 418  
Percent Similarity: 99.76% Conservative: 0  
Best Local Similarity: 99.76% Mismatches: 0  
Query Match: 99.27% Indels: 1  
DB: 6 Gaps: 1

US-09-377-795-2 (1-419) x CA916723 (1-1962)

Qy 1 MetanArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
Db 126 ATGAATAGGACCTCTCGAAGACCACTGTGTGAGATGTCAGCCAGTGGTGGCCGG 185

Qy 21 AlaAlaaspGlnAspValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40  
Db 186 GCAGCAGATCAGGACGTACTGGGCGAAGAGTCTCTCTGGGGAAGCCAGCCATGCTGCAC 245

Qy 41 LeuProSerGlnGlnAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60  
Db 246 CTGCTTCAGAACAGGGCGCTCTTGAGACCTCCAGCGCTGCTGGAGAGATCAAGAG 305

Qy 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluLeuLeu 80  
Db 306 CTCGAGATGCCATCCGGCAGACCAACCAAGATTCCTGGGAGCGCTGCGAGAGCTTCTG 365

Qy 81 HisPheGlnAlaSerGlnArgGluGlyGluPheLeuMetCysLysPheGlnGluAla 100  
Db 366 CATTTCCAGCCAGCCAGAGGAGGAGAGAGTTCCTCATGTGCAAGTTCAGAGAGGCC 425

Qy 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120  
Db 426 AGCAAACTGTGGAGAGACTCGCCCTGGAGAGCTCGATCTGAAGAGCCAGAGAGAGAG 485

Qy 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAla 140  
Db 486 GCTCTCGGGAGGTGAGACCTCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 542

Qy 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGluSerGlnSerArgLeu 160  
Db 543 TCTGTGAAGCCAGGTGACGTCTTGTCTGGGGAGCTGCAGGAGCCAGAGTCGCTTGT 602

Qy 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180  
Db 603 GAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGCTCGGGCCCGGCGCCAGCGAGCAG 662

Qy 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200  
Db 663 GCGCGCAGCTGGAGAGTGAGCGCGAGCGCTGCGAGCAGCAGCAGCGCTGCGAGGTGGAC 722

Qy 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220  
Db 723 CAGCTGCGCATGCGAGGCGCAGAGCGTGGAGCGCGCTCCGATGAGGAGCGCCAGCGCGCC 782

Qy 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaIleTyrHisGlnLeuPheGlnGlu 240  
Db 783 TCGGAGGAGAAAGAGAGAGCTGGCCAGTTGCGAGTGGCTATCACAGCTCTTCCAAGAA 842

Qy 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260  
Db 843 TACGACCAACCATCAAGAGCAGCGTGTGGCAGTGGAGCGGAAGCGAGGAATGCGAGT 902

Qy 261 GluAspLeuLysGlnGlnLeuGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280  
Db 903 GAAGATCTCAAAACAGCAGCTCCAGCAGCGCCGAGGAGGCGCTGGTGGCCAAACAGGAGGTG 962

Qy 281 IleAspLysLeuLysGluGluAlaGlnHisLysIleValMetGluThrValProVal 300  
Db 963 ATCATAGCTGAAGAGGAGGCGCAGCAGCAGCAAGATTGTGATGAGACCTTCCGGTG 1022

Qy 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320  
Db 1023 CTGAGGCCCGAGCGGATATCTACAGCGGAGCTTCAGGCTGAGAGGAGCCCGGGAG 1082

Qy 321 LysLeuAlaGluLysLysGluLeuGlnGlnGlnLeuGlnGlnLeuGlnArgGluTyr 340  
Db 1083 AAGCTGGCCGAGAAGAGGAGCTCTTCAGGAGCAGCTGGAGCAGCTGCGAGGAGGTAC 1142

Qy 341 SerLysLeuLysAlaSerCysGlnGluSerAlaArgIleGluAspMetArgLysArgHis 360  
Db 1143 AGCAACTGAAGGCCAGCTGTTCAGAGTGGCGCAGGATCGAGGACATGAGGAAGCGGCAT 1202

Qy 361 ValGluValSerGlnAlaProLeuProAlaProAlaProAlaTyrLeuSerSerProLeuAla 380  
Db 1203 GTCCAGGTCTCCAGGCCCCCTTCGCCCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1262

Qy 381 LeuProSerGlnArgArgSerProGluGluProProAspPheCysCysProLysCys 400  
Db 1263 CTGCCCCAGCAGAGGAGGAGCCCCCGGAGGAGCCACTGACTTCTGCTGCTGCTGCTG 1322

Qy 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419  
Db 1323 CAGTATCAGGCCCTGTATATGGACACCTTCAGATACATGTCAGTGTGATTGAG 1379

RESULT 4  
CR604149  
LOCUS full-length cDNA clone CS0DE005YJ20 of Placenta of Homo sapiens  
DEFINITION full-length cDNA clone CS0DE005YJ20 of Placenta of Homo sapiens (human).  
ACCESSION CR604149  
VERSION CR604149.1 GI:50484956  
KEYWORDS HTC; CNSLT; cDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1. (bases 1 to 1943)  
Li, W.B., Gruber, C., Jesses, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1943)  
REFERENCE 2 (bases 1 to 1943)  
Genoscope.

**TITLE**  
JOURNAL

**COMMENT**  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

**FEATURES**  
Location/Qualifiers  
Source  
1..1943  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DE005YJ20"  
/tissue\_type="Placenta"  
/plasmid="pCMVSPORT\_6"

**ORIGIN**

Alignment Scores:  
Pred. No.: 2e-179 Length: 1943  
Score: 2086.50 Matches: 419  
Percent Similarity: 99.52% Conservative: 0  
Best Local Similarity: 99.52% Mismatches: 0  
Query Match: 98.65% Indels: 2  
DB: 3 Gaps: 1

US-09-377-795-2 (1-419) x CR604149 (1-1943)

QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
DB 137 ATGAATAGGACCTCTGGAGAGCCAACTGTGTGAGATGTGTCAGCCAGTGTGGCCCG 196

QY 21 AlaAlaAspGlnAspValLeuGlyGluGlnSerProLeuGlyLysProAlaMetLeuHis 40  
DB 197 GCAGCAGATCAGACGCTACTGGCGGAAGAGTCTCTCTGGGAAGCCAGCCATGTGCAC 256

QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGlnAsnGlnGlu 60  
DB 257 CTGCCTTCAGACAGGCGCTCTCGAGACCTCCAGCGCTGCTGGAGAGATCAAGAG 316

QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80  
DB 317 CTCGAGATGCCATCCGCGAGAGCAACACAGATTCCTGCGGAGCGCTGCGAGGCTTCG 376

QY 81 HisPheGlnAlaSerGlnArgGluGlyGluPheLeuMetCysLysPheGlnGluAla 100  
DB 377 CATTTCCAGCCAGCCAGAGGAGGAGAGGAGTTCCTCATGTGCAAGTTCAGAGAGGCC 436

QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120  
DB 437 AGGNAACCTGGTGAGAGACTCGCCCTGGAGAGCTCGATCTGAGAGGCGAGAGGAGAG 496

QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140  
DB 497 GCTCTGCGGAGTGGAGCACCCTGAAGAGATGCCAGCAGCAGATGCTGAGGACAGGCC 556

QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160  
DB 557 TCTGTGAAGCCAGGTGACGCTCTGTCTGGGGAGCTGCGAGAGCCAGAGTGCCTTG 616

QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180  
DB 617 GAGGCTGCCACTNAGGATGCCAGGCTCTGGAGGGTGGGCGCGCGCCAGCAGAGAG 676

QY 181 AlaArgGlnLeuGlnSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200  
DB 677 GCGCGCAGCTGGAGAGTGGAGCGAGGCGCTGCGAGCAGCAGCAGCAGCTGAGGTGGAC 736

QY 201 GlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220  
DB 737 CAGCTGCGCATGACGGCCAGAGCGTGGAGGGCGCGCTCCGATGAGCGCAGCGCCGCC 796

QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240  
DB 797 TCGGAGGAGAGAGAGAGCTGCCCCAGTTTGCAGGTGGCCCTATCACCAGCTCTTCCAAGAA 856

QY 241 TyrAspAsnHisIleLysSerSerValValGlyLysArgLysArgLysArgLysArgLys 259  
DB 857 TAGCAACACCATCAAGAGCAGCGTGGTGGCAGTGAGCGGAAGCAGTGAAGGAATGCA 916

QY 259 nLeuGluAspLeuLysGlnGlnGlnAlaGluGluAlaLeuValAlaLysGlnGln 279  
DB 917 GCTGGAAGATCTCAAAACAGCAGCTCAGCAGGCGCCAGGAGGCGCTGGTGGCCCAACAGGA 976

QY 279 uValIleAspLysLeuLysGluGluAlaGlnHisLysIleValMetGluThrValPr 299  
DB 977 GGTGATCGATAAGCTGAAGGAGGAGCGCCGAGCAGCAGCAGAGATTGTGATGAGACCCCTTCC 1036

QY 299 oValLeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaAr 319  
DB 1037 GGTGCTGAAGCCCGAGCGGATATCTACAAGCGGAGCTTCCAGGCTGAGAGCGAGCGCCG 1096

QY 319 gGluLysLeuAlaGluLysLysGluLeuGlnGlnGlnGlnGlnGlnGlnGlnGln 339  
DB 1097 GGAGAAGCTGGCCGAGAGAGAGAGCTCTCTGAGGAGCAGCTGGAGCAGCTGCGAGAGGA 1156

QY 339 uTyrSerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysAr 359  
DB 1157 GTACAGCAAACTGAAGGCCAGCTGTCCAGAGTCCGCCAGGATCGAGGACATGAGGAAGCG 1216

QY 359 ghisValGluValSerGlnAlaProLeuProProAlaTyrLeuSerSerProLe 379  
DB 1217 GCATGTCGAGGTCTCCAGGCGCCCTTGCCCCCGCCCTGCTCTCTCTCTCTCTCTCTCT 1276

QY 379 uAlaLeuProSerGlnArgArgSerProGluGluProProAspPheCysProLys 399  
DB 1277 GGCCCTGCCAGCAGAGAGAGGAGGCCCCCCCCGAGGAGCCCTGACTTCTGCTGTCCCCAA 1336

QY 399 sCysGlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleG 419  
DB 1337 GTGCCAGTATCAGGCCCCCTGATATGACACCTGCGAGATACATGTCATGAGTGCATTGA 1396

QY 419 u 419  
DB 1397 G 1397

**RESULT 5**  
CR603029  
LOCUS  
DEFINITION  
full-length cDNA clone CS0DC017YA10 of Neuroblastoma Cot  
25-normalized of Homo sapiens (human).  
ACCESSION  
CR603029.1 GI:50483836  
VERSION  
HTC; CNSLT\_cDNA.  
KEYWORDS  
Homo sapiens (human)  
SOURCE  
Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 1751)  
AUTHORS  
Li,W.B., Gruber,C., Jesse,J., and Polayes,D.  
TITLE  
Full-length cDNA libraries and normalization  
JOURNAL  
Unpublished  
REMARK  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1751)  
Genoscope.  
Direct Submission  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

division of Invertebrates  
Location/Qualifiers  
source  
1. 1751  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS00C017A10"  
/tissue\_type="Neuroblastoma Cot 25-normalized"  
/plasmid="PCMVSPORT\_6"

## ORIGIN

Alignment Scores:  
Pred. No.: 4,76e-157 Length: 1751  
Score: 1840.50 Matches: 368  
Percent Similarity: 87.83% Conservative: 0  
Best Local Similarity: 87.83% Mismatches: 0  
Query Match: 87.02% Indels: 51  
DB: 3 Gaps: 1

US-09-377-795-2 (1-419) x CR603029 (1-1751)

QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyPro 20  
DB 128 ATGAATAGGACCTCTGGAGAGCCAACTGTGTGAGATGGTGCAGCCAGTGGTGGCCG 187  
QY 21 AlaAlaAspGlnAspValLeuGluGluSerProLeuGlyLysProAlaMetLeuHis 40  
DB 188 GCAGCAGATCAGGACGCTACTGGCGGAGAGTCTCTCTGGGAGACCCAGCCATGCTGCAC 247  
QY 41 LeuProSerGluGlnAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60  
DB 248 CTCGCTTCAGAACAGAGCGCTCTGAGACCTCCAGCGCTGCCTGAGGAGCAATCAAGAG 307  
QY 61 LeuArgAspAlaIleArgGlnSerLeuGluGluGluLeuArgCysGluGluLeuLeu 80  
DB 308 CTCGAGATGCCATCCGCGAGAGCAACAGATCTCTGGCGAGCGCTGCGAGAGCTCTG 367  
QY 81 HisPheGlnAlaSerGlnArgGluGluGluPheLeuMetCysLysPheGlnGluAla 100  
DB 368 CATTTCCAGCCAGCCAGAGGAGGAGGAGTCTCTCATGTGCAGTTCAGAGAGGCC 427  
QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGln 120  
DB 428 AGAAACTGGTGGAGAGACTCGCGCTGGAGAGCTCGATCTGAAGAGGAGCAGAGGAGCAG 487  
QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140  
DB 488 GCTCTGCGGAGGTGGAGCACCCTGAAGATGCCAGCAGATGGCTGAGGACAGGCC 547  
QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGluSerArgLeu 160  
DB 548 TCTGTGAAGCCAGGTGACGCTCTCTGCTCGGGAGCTGCGAGGAGCCAGAGTCGCTTG 607  
QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluArgAlaArgAlaAlaSerGluGln 180  
DB 608 GAGGTGCCACTAGAGATGCCAGGCTCTGGAGGCTCGG----- 646  
QY 181 AlaArgGlnLeuGluSerGluGluAlaLeuGlnGlnHisSerValGlnValAsp 200  
DB 646 ----- 646  
QY 201 GlnLeuArgMetGlnGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220  
DB 646 ----- 646  
QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaThrHisGlnLeuPheGlnGlu 240  
DB 647 -----AGGAAGCTGGCCAGTTCGAGGTGGCTATACACAGCTCTTCCAGAA 694  
QY 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260  
DB 695 TACGACAAACCATCAAGAGCAGCGTGTGGGAGTGCAGCGGAGGAGGAGGAGTGCAGCTG 754

QY 261 GluAspLeuLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280  
DB 755 GAAGATCTCAACAGCAGCTCCAGCAGCCGAGGAGGCCCTGGTGGCCAAACAGAGGAGTG 814  
QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300  
DB 815 ATCATTAAGCTGAAGGAGGAGGCCGAGCAGCACAAGATTGTGATGGAGACCTTCGGGTG 874  
QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320  
DB 875 CTGAAGGCCCGAGCGGATATCTACAGCGGAGCTTCAGGCTGAGAGCAGGCCCGGAG 934  
QY 321 LysLeuAlaGluLysLysGluLeuGlnGlnGlnLeuGlnGlnLeuGlnArgGluTyr 340  
DB 935 AAGCTGGCCGAGAGAAGAGGAGCTCTGTCAGGAGCAGCTGGAGCAGCTCAGAGGAGTAC 994  
QY 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgIleGluAspMetArgLysArgHis 360  
DB 995 AGCAACTGAGGCCAGCTGTGAGGATGCGGCCAGGATCGAGGACATGAGGAAGCGCAT 1054  
QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaTyrLeuSerSerProLeuAla 380  
DB 1055 GTCGAGGTCTCCAGAGGCCCTTGGCCCGCCCTGCTACCTCTCTCTCTCTCTCTCTG 1114  
QY 381 LeuProSerGlnArgArgSerProGluGluProProAspPheCysCysProLysCys 400  
DB 1115 CTGCCCCAGCAGAGGAGGAGGCCCGCCCGAGGAGCAGCTGACTTCTGCTGTCTCCCAAGTGC 1174  
QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419  
DB 1175 CAGTATCAGGCCCTTGATATGAGCACCTCGAGATACATGTATGAGTGCATTGAG 1231

RESULT 6  
AK037020 4535 bp mRNA linear HTC 03-APR-2004  
LOCUS Mus musculus adult female vagina cDNA, RIKEN full-length enriched  
DEFINITION library, clone:9930039F20 product:unknown EST, full insert  
sequence.  
ACCSSION AK037020  
VERSION AK037020.1 GI:26331883  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
REFERENCE 2  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20493374  
PUBMED 11042159  
REFERENCE 3  
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kishinai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujitake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
TITLE RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861  
REFERENCE 4

**AUTHORS**  
**JOURNAL**  
**REFERENCE**  
**AUTHORS**

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)  
5  
The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 4535)

**TITLE**  
**JOURNAL**  
**REFERENCE**  
**AUTHORS**

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
Location/Qualifiers

**TITLE**  
**JOURNAL**

1. .4535  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="FANTOM DB:9930039F20"  
/db\_xref="taxon:10090"  
/clone="9930039F20"  
/sex="female"  
/tissue\_type="vagina"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
136. .1371  
/note="unnamed protein product; putative unknown EST (GB|BB646967, evidence: BLASTN, 99%, match=720)"  
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/protein\_id="BAC29672.1"  
/db\_xref="GI:26331884"  
/translation="MNKHFWKQLSEMVDPGPAEDQMLGESLSLGPAMHLHPSE QGTPETLQCELENDRAIRSNQMLRERCEELHVFQVSRERKEFLMCKFPQARK LVERLSLEKRSQREQLKELEQLKKQCAEDKASVKAQVTSLLGELOESQRLE AATKQDALEGRIRAVSEVROLESERVLQOQHSVQVDLQRMQNSVEAALMERQQA ASEERKKAQQAQVHOLFQDYDSHKKSKGQVLEDLQQLQQAQEAALVAKQELDKL KEAQKHQKLVMEVPLVKQAQADLYKADFOERHAREKLVVEKKEYLOEQLQREBFNK LKVGCHESARIEDMRKRHVETPPPLLPAPAHSHFLALSNNRSPPEPPDFCCPKC QYQAPDMDTLQIHVMECIE"

**FEATURES**  
**source**

polya\_signal  
4515. .4520  
/note="putative"  
polya\_site  
4535  
/note="putative"

**ORIGIN**  
**Alignment Scores:**

1012 TTGAAGGCCCGAGCGGATATCTACAAGGCTGACTTCCAAAGCTGAGAGGCGATGCCCGGAG 1071

**Pred. No.:**  
**Score:**  
**Percent Similarity:**  
**Best Local Similarity:**  
**Query Match:**  
**DB:**

5.63e-154 Length: 4535  
1813.00 Matches: 362  
90.93% Conservative: 19  
86.40% Mismatches: 30  
85.72% Indels: 8  
3 Gaps: 2

US-09-377-795-2 (1-419) x AK037020 (1-4535)

QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
DB 136 ATGAACAAGCACCCCTGGGAAGAACCCAGCTGAGTGGATGGTGGAGCCCTGGTGGCCCA 195  
QY 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40  
DB 196 GCAGAGGACCAGGACATGCTGGGTGAGAAATCTTCTCTGGGAGAGCTGCATGCTACAT 255  
QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60  
DB 256 CTGCCTTCAGACGAGGCTACTCTGAGACCTCCAGCGCTGCTGGAAGAGATCAAGAG 315  
QY 61 LeuArgAspAlaIleArgGlnSerHisGlnIleLeuArgGluArgCysGluGluLeuLeu 80  
DB 316 CTCGAGAGCGCTATCCGGCAGAGCAATCAGATGCTGAGGGAACGCTGTGAGGAGCTGCTG 375  
QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100  
DB 376 CATTTCCAGTCAGCCGCGGAGGAGAGAGTCTTATGTGCANAATTCAGGAGGCC 435  
QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLysArgGlnLysGluGln 120  
DB 436 CGCAAGCTGGTGGAGAGACTGAGCTTGGAGAAGCTTGATCTTCGAGTCCAGAGGGAACAG 495  
QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140  
DB 496 GCCTTAAAGGAGTGGAGCAACTGAAGAAATGC---CAACAGATGCTCAGGAGCCAGAGGCC 552  
QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160  
DB 553 TCTGTGAAGCTCAGTGACATCATCTGCTCGAGGAATCTCAGGAGCCAGAGCCGCTTTG 612  
QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180  
DB 613 GAGGCTGCCACCAAGATCGGCAAGCTTTAGAGGGAAGGATTCGAGCAGTTAGTGAGCAG 672  
QY 181 AlaArgGlnLeuLysSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200  
DB 673 CTCAGACAGCTGGAGAGTGAGCGGAGGTGCTTACAGCAGCAGCAGCGTCCAGGTGGAC 732  
QY 201 GlnLeuArgMetGlnGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAla 220  
DB 733 CAGCTCGGTATGCCAACCCAGAGCGTGGAGGCTGCTTCCGAATGGAGCGGCGAGGCTGCT 792  
QY 221 SerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGlnGlu 240  
DB 793 TCAGAGGAGAGCGGAAGCTGCTCAGTTGTCAGGCGAGCCCTATCACCAGCTCTTCCAAGAC 852  
QY 241 TyrAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnLeu 260  
DB 853 TACGACAGCACATTAAGCAGCAGC-----AAGGCGCATGCAGCTG 891  
QY 261 GluAspLeuLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLysGlnGluVal 280  
DB 892 GAAGATCTGAGGCAACAGCTCCAGCAAGCTGAGGAGGCCCTGGTGAAGAGCAAGAAATTT 951  
QY 281 IleAspLysLeuLysGluGluAlaGluGlnHisLysIleValMetGluThrValProVal 300  
DB 952 ATTGATAAGCTCAAGAGAGGAGGCTGAGCAGCAGCAAGATTTGTGATGGAGACTGTGCCAGTC 1011  
QY 301 LeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArgGlu 320  
DB 1012 TTGAAGGCCCGAGCGGATATCTACAAGGCTGACTTCCAAAGCTGAGAGGCGATGCCCGGAG 1071

QY 321 LysLeuAlaGluLysLysGluLeuLeuGlnGluLeuGlnGlnLeuGlnArgGluTyr 340  
 Db 1072 AAGCTGTGGAGAGAGAGAGTATTTCAGAGAGAGCTGGAGCAGCTGGAGCGCGAGTTC 1131  
 QY 341 SerLysLeuLysAlaSerCysGlnGlnSerAlaArgileGluAspMetArgLysArgHis 360  
 Db 1132 AACAAAGCTGAAGTTGGCTGCCATGAGTCAGCCAGGATTGAGGATATGAGGAAGCGCAT 1191  
 QY 361 ValGluValSerGlnAlaProLeuProAlaProAlaProAlaTyrLeuSerSerProLeuAla 380  
 Db 1192 GTAGAGACTCCCAAGCCTCTTACTCCCTGCTCCAGCTCACACCTCTTTCAATTGGCC 1251  
 QY 381 LeuProSerGlnArgSerProGluGluProProAspPheCysCysProLysCys 400  
 Db 1252 TTGTCCAAACAGCGAGAGCCCTCTCTGAAGAACCTCTGACTTCTGTGTTCGAGAGTGC 1311  
 QY 401 GlnTyrGlnAlaProAspMetAspThrLeuGlnIleHisValMetGluCysIleGlu 419  
 Db 1312 CAGTATCAGGCTCCTGATATGGACACTACAGATACATGTCATGAGTGTCATAGAG 1368

## RESULT 7

BX332283

LOCUS

DEFINITION BX332283 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens  
 cDNA clone CS0DC010YF13 5-PRIME, mRNA sequence.

ACCESSION

BX332283

VERSION

BX332283.2

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

On May 2, 2003 this sequence version replaced gi:30339089.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

10873.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?e=CS0DC010CC07QF1&c=10873.f.

## FEATURES

source

1. .1118

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DC010YF13"

/tissue\_type="NEUROBLASTOMA COT 25-NORMALIZED"

/clone\_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo (dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

## Alignment Scores:

Pred. No.: 2,82e-118 Length: 1118  
 Score: 1412.50 Matches: 309  
 Percent Similarity: 93.96% Conservative: 2  
 Best Local Similarity: 93.35% Mismatches: 17  
 Query Match: 66.78% Indels: 7  
 DB: 5 Gaps: 0

US-09-377-795-2 (1-419) x BX332283 (1-1118)

QY 1 MetAenArgHisLeu-TrpLysSerGlnLeuMetValGlnProSerGlyGlyPr 20  
 Db 96 ATGAATAGGCACCTTCTGGAAGAGCCAACTGTGTGAGATGTCAGCCAGTGTGTGGCCC 155  
 QY 20 oAlaAlaAspGlnAspValLeuGluGluSerProLeuGlyLysProAlaMetLeuHi 40  
 Db 156 GCGAGCAGATCAGGAGCTACTGGGCGAAGAGTCTCTCTGGGGAAGCAGCAGCATCTGCA 215  
 QY 40 sLeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGl 60  
 Db 216 CTGCTTTCAGAACAGGCGCTCTCTGAGACCTCTCAGCGCTGCTTGGAGGAGATCAAGA 275  
 QY 60 uLeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLe 80  
 Db 276 GCTCCGAGATGCCATCCGGCAGAGCAACCAAGATTCTGCGGAGCGCTGCGAGGAGCTTCT 335  
 QY 80 uHisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAl 100  
 Db 336 GCATTTCCAGCCAGCCAGAGGGAGGAGAGAGTTCCTCATGTGCAAGATTCCAGGAGGC 395  
 QY 100 aArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGl 120  
 Db 396 CAGGAACCTGCTGGAGAGACTCGGCTTGGAGAGCTCGATCTGAAGAGCGCAGAGGAGCA 455  
 QY 120 nAlaLeuArgGluValGluHisLeuLysArgCysGlnGlnMetAlaGluAspLysAl 140  
 Db 456 GGCTCTCGGGAGGTGGAGCACCTGAAGATGCCAGCAGCAGATGCTGAGGACAGGC 515  
 QY 140 aSerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLe 160  
 Db 516 CTCTGTGAAGCCAGCGTGAAGTCTTGTCTGGGAGCTGCGAGGAGCGCAGAGTCTGCTT 575  
 QY 160 uGluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGl 180  
 Db 576 GSAGGCTGCCACTAAGAAATGCCAGGCTCTGGAGGCTCGGGCCCGCGGCGCAGCGAGCA 635  
 QY 180 nAlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGln-Vala 200  
 Db 636 GGGCGGCGAGCTGGAGAGTGAGCGGAGGCGCTGCGAGCAGCAGCAGCGTGCAGGGTGG 695  
 QY 200 spGlnLeuArgMetGlnGlnGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaA 220  
 Db 696 ACCAGCTGGCGCATGAGGCGCAGAGCGTGGAGCGCGCTCCGATGAGCCCGAGGCGCG 755  
 QY 220 lAserGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyrHisGlnLeuPheGln 240  
 Db 756 CCTCGAGGAGAGAGAGAGTGGCCAGTTGCGAGTGGCTATCACCACTCTTCCAAG 815  
 QY 240 lutyAspAsnHisIleLysSerSerValValGlySerGluArgLysArgGlyMetGlnL 260  
 Db 816 AATACGACCAACCATCAAGAGCAGCGTGTGGGCGAGTGGCGGAGCAGGTGAATGAGC 875  
 QY 260 euGluAspLeuLysGlnGlnLeuGlnGlnAlaGluAlaLeuValAlaLysGlnGluV 280  
 Db 876 TGGAGATCTCAA-CAGCAGCTCCAGCAGCGCGAGGAGCGCTGTGTGGCCAAACAGAGG 934  
 QY 280 aIleAspLysLeuLysGluGluAlaGluGlnHisLysIle-ValMetGluThrValPro 299  
 Db 935 TGAATGATGAAGTGAAGGAGGAGCGAGCMGACCAAGATTCTTAATGGAGACAGTCCCG 994  
 QY 300 ValLeuLysAlaGlnAlaAspIleTyrLysAlaAspPheGlnAlaGluArgGlnAlaArg 319  
 Db 995 GTGCTGAAGCC-CAGGSGGATATCTWMAAGGGGAGCTTCAG-GCTGAGAGGMA-GCCCGG 1051  
 QY 320 GluLysLeuAlaGluLysLysGluLeu 328  
 Db 1052 GAAAGCTGGCGAGAAAAAGGAGSCCCTC 1078

## RESULT 8

AL545822

LOCUS

DEFINITION

AL545822

974 bp mRNA linear EST 25-MAR-2004

Clone CS0DI023YC04 5-PRIME, mRNA sequence.

```

ACCESSION AL545822
VERSION AL545822.3 GI:45746298
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 974)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31267657.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
10873.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DEI0238B02QP1&c=10873.f.
FEATURES
source
1. .974
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI023YC04"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Alignment Scores:
Pred. No.: 4,19e-110 Length: 974
Score: 1322.00 Matches: 275
Percent Similarity: 97.54% Conservative: 2
Best Local Similarity: 96.83% Mismatches: 5
Query Match: 62.51% Indels: 3
DB: 1 Gaps: 0
US-09-377-795-2 (1-419) x AL545822 (1-974)
QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
Db 126 ATGATAGGCACCTCTGGAARAGCCAACTGTGTGARATGTTGCAGCCCACTGTGGCCCG 185
QY 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40
Db 186 GCAGCAGATCAGGACGCTACTGGCGGAAGAGTCTCTCTCGGGAAGCCAGCCATGTCGCAC 245
QY 41 LeuProSerGluGlnGlnValAlaProGluThrLeuGlnArgCysLeuGluGlnGlnGlu 60
Db 246 CTGCTTCAGAACAGGGCGCTCTGAGACCCCTCCAGCGCTGCTGAGGAGAGATCAAGAG 305
QY 61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80
Db 306 CTCGAGATGCCATCCGGCAGACCAACAGATTCTGCGGAGCGCTGCGAGGAGCTTCTG 365
QY 81 HisPheGlnAlaSerGlnArgGluGluLysGluPheLeuMetCysLysPheGlnGluAla 100
Db 366 CATTTTCAAGCCAGCCAGAGGAGGAGAGAGGAGTTCTCTATGTCGAAGTTCCAGGAGGCC 425
QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnGlnGln 120
Db 426 AGGAAACTCGTGAGAGACTCGCGCTGGGAGAGCTGATCTGAAGAGGAGGAGGAGCAG 485
QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140

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Db 486 GCTCTGCGGGAGGTGGAGCACCTGAAGAGATGCCAGCAGCAGATGCTGAGCACAAGGCC 545
QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160
Db 546 TCTGTGAAGCCAGGTGACGTCCTTGTCTGGGGAGCTGCAGGAGAGCCAGAGTGCCTTG 605
QY 161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
Db 606 GAGGTGCTCCACTAAGGATGCCAGGCTCTGGAGGGTTCGGGCCCGGGCCAGGAGCAG 665
QY 181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGln-ValAs 200
Db 666 GCGCGCAGCTGGAGAGTGAGCGCGCTGCAGCAGCAGCAGCAGCAGCTGCAGGGTGA 725
QY 200 pGlnLeuArgMetGlnGlyGlnSerValGluAlaAlaLeuArgMetGluArgGlnAla 220
Db 726 CCAGCTGCGCATGCGAGGGCCAGAGGCTGGAGCGCGCTCCGATGGAGSCCAGGGCCGC 785
QY 220 sSerGlu-GluLysArgLysLeuAlaGlnLeuGlnValAlaValAlaValHisGlnPheGln 240
Db 786 CTCGGAGGGAGAGAGAGCTGGSCCAGTTGCAGGTGGCCTATCACCAGCTCTTCCAAG 845
QY 240 luTyAspAsnHisIleLysSerValValGlySerGluArgLysArgGlyMetGlnL 260
Db 846 AATACGACAAACCATCAAGAGCAGCGTGGTGGCAGTGAGCGGAASAGYGAATGCAGC 905
QY 260 euGluAspLeuLysGlnGlnGlnGlnAlaGluGluAlaLeuValAlaLysGlnGlu 280
Db 906 TGGAGATCTCAACAGCAGCTCCAGCAGCGCGGAGGAGGCGCTGGTGGTGGC-AAACAGGAG 964
QY 280 alIleAsp 282
Db 965 TGATCGAT 972
RESULT 9
AL541141
LOCUS
DEFINITION AL541141 Homo sapiens PLACENTA Homo sapiens cDNA clone EST 24-MAR-2004
5-PRIME, mRNA sequence.
ACCESSION AL541141
VERSION AL541141.3 GI:45716735
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1043)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:30545027.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 10873.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DE005DE10QP1&c=10873.f.
FEATURES
source
1. .1043
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE005Y020"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed

```

with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

## ORIGIN

## Alignment Scores:

Pred. No.: 7,84e-109 Length: 1043  
Score: 1308.50 Matches: 278  
Percent Similarity: 95.25% Conservative: 3  
Best Local Similarity: 94.24% Mismatches: 13  
Query Match: 61.87% Indels: 5  
DB: 1 Gaps: 0

US-09-377-795-2 (1-419) x ALS41141 (1-1043)

QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20  
DB 139 ATGAATAGGACCTCTGGAAGACCACTGTGTGAGATGTCAGCCAGTGTGGCCGG 198  
QY 21 AlaAlaAspGlnAspValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40  
DB 199 GCAGCAGATCAGGACCTACTGGCGGAAGAGTCTCTCTGGGGAAGCCAGCCATGCTGCAC 258  
QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60  
DB 259 CTGCTTCAGAACAGGCGCTCTGAGACCTCCAGCGCTGCTGGAGAGAAATCAAGAG 318  
QY 61 LeuArgAspAlaLeuArgGlnSerLeuGlnLeuLeuArgGluArgCysGluLeuLeu 80  
DB 319 CTCGAGATGCCATCCGCGAGACCAACAGATTCCTGCGGAGCGCTGCGAGAGCTTCGT 378  
QY 81 HisPheGlnAlaSerGlnArgGluGlyGluPheLeuMetCysLysPheGlnGluAla 100  
DB 379 CATTTCCAGCCAGCCAGAGGAGAGAGAGTTCCTCATGTGAAGTTCCAGAGGCC 438  
QY 101 ArgLysLeuValGluArgLeuGlyLeuGluLysLeuAspLeuLysArgGlnLysGluGln 120  
DB 439 AGAAACTGCTGGAGAGACTCGGCTGGAGAGTCTGATCTGAAGAGGACAGAGGACAG 498  
QY 121 AlaLeuArgGluValGluHisLeuLysArgCysGlnGlnGlnMetAlaGluAspLysAla 140  
DB 499 GCTTCGCGGAGGTGAGACCTCTGAAGAGATGCCAGCAGAGATGGCTGAGGACAGGCC 558  
QY 141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160  
DB 559 TCTGTGAAGGCCAGGTGAGTCTTCTGCTGGGAGCTGCGAGAGAGCCAGATGCTGTTG 618  
QY 161 GluAlaAlaThrLysGluCysGlnAlaLeu-GluGlyArgAlaAlaArgAlaLaserGluG 180  
DB 619 GAGGCTGCCACTAAGGAATGCCAGGCTCTGGADGGGTGGGCGCGCGCCAGCGAGCA 678  
QY 180 nAlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValas 200  
DB 679 GCGCGGCGAGCTGAGAGTGGCGGAGGSGTG-CAGCAGCR-CACAGCGTGCAGGTGGA 736  
QY 200 pGlnLeuArgMetGlnGlnSerValGluAlaAlaLeuArgMetGluArgGlnAlaAl 220  
DB 737 CCAGCTGGCGATCGCGGCGCAGAGCGTGGAGCGCGCTCGCATCGGATGASCAAGGCGCG 796  
QY 220 aSerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyHisGlnLeuPheGlnG 240  
DB 797 CTCGAGGAGAGAGAGAGTGGCGGCGAGTTCAGGTGGCGCTATCACCAGCTCTTCCAAGA 856  
QY 240 uTyRAspLeuHisLeuLysSerSerValValGlySerGluArgLysArgGlyMetGlnLe 260  
DB 857 ATACGACACACATCAAGACAGCGTGGTGGGAGTGAGCGGAGGAGGAGGATGAGCT 916  
QY 260 uGluAspLeuLysGlnGlnLeuGlnGlnAlaGluGluAlaLeuValAlaLysGlnGlu 280  
DB 917 GGAAGATCTCAAAACARCAAGCTCCAGCAGCGCGAGAGGCGCTGGTGGCMAAMAGAGGT 976  
QY 280 lIleAspLysLeuLysGluGluAlaGluGlnHisLysIleVal 294

Db 977 GATCGATAARCTGAAGGAGGG-GCCGAGMR-CACAAAATTTR 1017  
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RESULT 10  
BQ932422

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## COMMENT

## COMMENT

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## COMMENT

## COMMENT

BQ932422 957 bp mRNA linear EST 21-AUG-2002  
AGENCOURT\_8774276 NIH\_MGC\_43 Homo sapiens cDNA clone IMAGE:6375422  
5', mRNA sequence.

BQ932422  
BQ932422.1 GI:22347740

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 957)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LNCM2555 row: p column: 15

High quality sequence stop: 621.

Location/Qualifiers

1..957

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6375422"

/tissue\_type="normal pigmented retinal epithelium"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_43"

/notes="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally-

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Library constructed by Ling Hong

in the laboratory of Gerald W. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH\_MGC Library. |"

Alignment Scores:

Pred. No.: 7,24e-104 Length: 957

Score: 1253.50 Matches: 253

Percent Similarity: 95.86% Conservative: 2

Best Local Similarity: 95.11% Mismatches: 10

Query Match: 59.27% Indels: 1

DB: 5 Gaps: 1

US-09-377-795-2 (1-419) x BQ932422 (1-957)

QY 1 MetAsnArgHisLeuTrpLysSerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20

DB 124 ATGAATAGGACCTCTGGAAGACCACTGTGTGAGATGTCAGCCAGTGTGGCCGG 183

QY 21 AlaAlaAspGlnAspValLeuGlyGluGluSerProLeuGlyLysProAlaMetLeuHis 40

DB 184 GCAGCAGATCAGGACCTACTGGCGGAAGAGTCTCTCTGGGGAAGCCAGCCATGCTGCAC 243

QY 41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60

DB 244 CTGCTTCAGAACAGGCGCTCTGAGACCTCCAGCGCTGCTGGAGAGATCAAGAG 303

QY 61 LeuArgAspAlaIleArgGlnSerLeuGlnLeuArgGluArgCysGluGluLeuLeu 80

DB 917 GGAAGATCTCAAAACARCAAGCTCCAGCAGCGCGAGAGGCGCTGGTGGCMAAMAGAGGT 976

QY 280 lIleAspLysLeuLysGluGluAlaGluGlnHisLysIleVal 294





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RESULT 12
BM478785      1098 bp      mRNA      linear      EST 05-FEB-2002
LOCUS      AGENCOURT 6400582 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5526874
DEFINITION      5', mRNA sequence.
ACCESSION      BM478785
VERSION      BM478785.1 GI:18527827
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      1 (bases 1 to 1098)
TITLE      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL      NIH-MGC http://mgs.nci.nih.gov/.
COMMENT      National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/BTP
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12201 row: d column: 11
            High quality sequence stop: 612.

FEATURES             Location/Qualifiers
     source           1..1098
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5526874"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
                     Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
                     Average insert size 2 kb. Library constructed by Life
                     Technologies."

ORIGIN
Alignment Scores:
Pred. No.:      4,69e-103      Length:      1098
Score:          1245.50      Matches:      259
Percent Similarity: 91.64%      Conservative: 15
Best Local Similarity: 86.62%      Mismatches: 21
Query Match:    58.83%      Indels:      4
DB:             4              Gaps:        3

US-09-377-795-2 (1-419) x BM478785 (1-1098)

QY      1 MetAsnArgHisLeuTriPlySerGlnLeuCysGluMetValGlnProSerGlyGlyPro 20
DB      132 ATGATAGGCACCTCTGGAGAGCAACTGTGAGATGGTGACGACCATGTGTGCCCG 191
QY      21 AlaAlaAspGlnAspValLeuGlyGluSerProLeuGlyLysProAlaMetLeuHis 40
DB      192 GCAGCAGATCAGGAGCTACTGGGCGAGAGTCTCTCTGGGGAAGCCAGCATCTGTCAC 251
QY      41 LeuProSerGluGlnGlyAlaProGluThrLeuGlnArgCysLeuGluGluAsnGlnGlu 60
DB      252 CTGGCTTCAGAACAGGGCGCTCTGAGACCTCCAGCGCTCGCTGGAGGAGAAATCAAGAG 311
QY      61 LeuArgAspAlaIleArgGlnSerAsnGlnIleLeuArgGluArgCysGluGluLeuLeu 80
DB      312 CTCGAGATGTCATCCGCGAGAGCAACAGATTCTGGGAGGCGCTGGAGGAGCTTCG 371
QY      81 HisPheGlnAlaSerGlnArgGluGluGlySerPheLeuMetCysLysPheGlnGluAla 100
DB      372 CATTTCCAAAGCCAGCAGAGGAGGAGAGGAGTTCCTCATGTGCAAGTTCAGGAGGCC 431

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QY      101 ArgLysLeuValGluArgLeuGlyLeuGlyLysLeuAspLeuLysArgGlnLysGluGln 120
DB      432 AGGAAACTGGTGGAGAGACTCGGCTCGGAGAGCTCGATCTGAGAGGAGGAGGAGCAG 491
QY      121 AlaLeuArgGluValGluHisLeuLysLeuArgCysGlnGlnGlnMetAlaGluAspLysAla 140
DB      492 GCTCTGGGGAGGTGGAGCACCTGAAGAGATGCCAGCAGCAGATGGCTGAGGACAAGGCC 551
QY      141 SerValLysAlaGlnValThrSerLeuLeuGlyGluLeuGlnGlnSerGlnSerArgLeu 160
DB      552 TCTGTGAAGCCAGGTGACCTCTTCTCGGGAGCTGCGAGGAGCAGCAGATGCGCTTG 611
QY      161 GluAlaAlaThrLysGluCysGlnAlaLeuGluGlyArgAlaArgAlaAlaSerGluGln 180
DB      612 GAGGCTGCCACTAAGGAATGCCAGGCTCTGGAGGTCGGGCGCGCGCCAGCAGCAGCAG 671
QY      181 AlaArgGlnLeuGluSerGluArgGluAlaLeuGlnGlnGlnHisSerValGlnValAsp 200
DB      672 GCGCGGAGCTGGAGAGTGAGCGCGAGCGCTGCGAGCAGCAGCAGCAGCGTGCAGGTGAC 731
QY      201 GlnLeuArgMetGlnGlyGln-SerValGluAlaAlaLeuArgMetGluArgGlnAlaAl 220
DB      732 CAGCTGGCATGCGAGGCGCAGAAACGCTGGAGGCGCGCTCGCATGGAGCCCGCAGCAGC 791
QY      220 aSerGluGluLysArgLysLeuAlaGlnLeuGlnValAlaTyHisGlnLeuPheGlnG 240
DB      792 CTCGAGGGGAGAGAAGAGCTGCCAGTTGCAAGTGGCGCTATCACCAGCTCTTTCAAGA 851
QY      240 uTyAspAsnHisIleLysSerSerValValGlySerGlu---ArgLysArgGlyMetG 259
DB      852 ATAGCACCACCTCCAGAAACACCGCTGGTGGCAGTGAGCCGGAACCCAGAAATGCAC 911
QY      259 nLeuGluAspLeuGlnGlnLeuGlnAlaGluGluAlaLeuValAla---LysG 278
DB      912 CTGCAAAAATCTCAACAGCAGCTCCCAACAGGCAAGAAAGCCCTGGGGGCCCCAACCG 971
QY      278 nGluValIleAspLysLeu---LysGluGluAlaGluGlnHisLysIleValMet 295
DB      972 GGAGGGGGTCCAAAACCTTAAGGAGGGAGGAGGCAACACCACCAAAATTTGTGATT 1026

RESULT 13
AL558226      1024 bp      mRNA      linear      EST 02-APR-2004
LOCUS      AL558226 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
DEFINITION      Homo sapiens cDNA clone CS0DU001YH07 5-PRIME, mRNA sequence.
ACCESSION      AL558226
VERSION      AL558226.3 GI:46183625
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      1 (bases 1 to 1024)
TITLE      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL      Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
COMMENT      Full-length cDNA libraries and normalization
            Unpublished (2001)
            On Feb 15, 2001 this sequence version replaced gi:31280025.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            10873.f
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DU001CD04QP1sc=10873.f.
            Location/Qualifiers
            1..1024
            /organism="Homo sapiens"
            /mol_type="mRNA"

FEATURES             source

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QY 259 InLeuGluAspLeuLys 264  
|||:::|||||  
Db 799 AGCTGGATGATCTCAA 815

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Job time : 4395 secs

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